

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: QUENTIN-MILLET al., Marie-Jose et
- (ii) TITLE OF INVENTION: TBP2 FRAGMENTS OF THE TRANSFERRIN
RECEPTOR OF NEISSERIA MENINGITIDIS
- (iii) NUMBER OF SEQUENCES: 44
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: LARSON AND TAYLOR
(B) STREET: 1199 NORTH FAIRFAX STREET
(C) CITY: ALEXANDRIA
(D) STATE: VIRGINIA
(E) COUNTRY: USA
(F) ZIP: 22314
- CS (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/591,447
(B) FILING DATE: 29-JAN-1996
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: SARRO, THOMAS P
(B) REGISTRATION NUMBER: 19,196
(C) REFERENCE/DOCKET NUMBER: XI/P02956
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 703-739-4900
(B) TELEFAX: 703-739-9577

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2230 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: IM2169
- (ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 60..119
- (ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 120..2192

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 60..2192

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 120..1154

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1155..1748

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1749..2192

(ix) FEATURE:

(A) NAME/KEY: misc_binding

(B) LOCATION: 237..1169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATTTGTTAAA AATAAATAAA ATAATAATCC TTATCATTCT TTAATTGAAT TGGGTTTAT	59
ATG AAC AAT CCA TTG GTA AAT CAG GCT GCT ATG GTG CTG CCT GTG TTT	107
Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe	
-20 -15 -10 -5	
TTG TTG AGT GCC TGT CTG GGC GGC GGC GGC AGT TTC GAT CTT GAT TCT	155
Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser	
1 5 10	
GTC GAT ACC GAA GCC CCG CGT CCC GCG CCA AAG TAT CAA GAT GTT TCT	203
Val Asp Thr Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser	
15 20 25	
TCC GAA AAA CCG CAA GCC CAA AAA GAC CAA GGC GGA TAC GGT TTT GCG	251
Ser Glu Lys Pro Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala	
30 35 40	
ATG AGG TTG AAA CGG AGG AAT TGG TAT CCG GGG GCA GAA GAA AGC GAG	299
Met Arg Leu Lys Arg Arg Asn Trp Tyr Pro Gly Ala Glu Glu Ser Glu	
45 50 55 60	
GTT AAA CTG AAC GAG AGT GAT TGG GAG GCG ACG GGA TTG CCG ACA AAA	347
Val Lys Leu Asn Glu Ser Asp Trp Glu Ala Thr Gly Leu Pro Thr Lys	
65 70 75	
CCC AAG GAA CTT CCT AAA CGG CAA AAA TCG GTT ATT GAA AAA GTA GAA	395
Pro Lys Glu Leu Pro Lys Arg Gln Lys Ser Val Ile Glu Lys Val Glu	
80 85 90	
ACA GAC GGC GAC AGC GAT ATT TAT TCT TCC CCC TAT CTC ACA CCA TCA	443
Thr Asp Gly Asp Ser Asp Ile Tyr Ser Ser Pro Tyr Leu Thr Pro Ser	
95 100 105	

AAC Asn 110	CAT His	CAA Gln	AAC Asn	GGC Gly	AGC Ser	GCT Ala 115	GGC Gly	AAC Asn	GGT Gly	GTA Val	AAT Asn 120	CAA Gln	CCT Pro	AAA Lys	AAT Asn	491
CAG Gln 125	GCA Ala	ACA Thr	GGT Gly	CAC His	GAA Glu 130	AAT Asn	TTC Phe	CAA Gln	TAT Tyr	GTT Val 135	TAT Tyr	TCC Ser	GGT Gly	TGG Trp	TTT Phe 140	539
TAT Tyr	AAA Lys	CAT His	GCA Ala	GCG Ala 145	AGT Ser	GAA Glu	AAA Lys	GAT Asp	TTC Phe 150	AGT Ser	AAC Asn	AAA Lys	AAA Lys	ATT Ile 155	AAG Lys	587
TCA Ser	GGC Gly	GAC Asp 160	GAT Asp	GGT Gly	TAT Tyr	ATC Ile	TTC Phe 165	TAT Tyr	CAC His	GGT Gly	GAA Glu	AAA Lys	CCT Pro 170	TCC Ser	CGA Arg	635
CAA Gln	CTT Leu	CCT Pro 175	GCT Ala	TCT Ser	GGA Gly	AAA Lys	GTT Val 180	ATC Ile	TAC Tyr	AAA Lys	GGT Gly	GTG Val 185	TGG Trp	CAT His	TTT Phe	683
GTA Val 190	ACC Thr	GAT Asp	ACA Thr	AAA Lys	AAG Lys	GGT Gly 195	CAA Gln	GAT Asp	TTT Phe	CGT Arg	GAA Glu 200	ATT Ile	ATC Ile	CAG Gln	CCT Pro	731
TCA Ser 205	AAA Lys	AAA Lys	CAA Gln	GGC Gly	GAC Asp 210	AGG Arg	TAT Tyr	AGC Ser	GGA Gly	TTT Phe 215	TCT Ser	GGT Gly	GAT Asp	GGC Gly	AGC Ser 220	779
GAA Glu	GAA Glu	TAT Tyr	TCC Ser	AAC Asn 225	AAA Lys	AAC Asn	GAA Glu	TCC Ser	ACG Thr 230	CTG Leu	AAA Lys	GAT Asp	GAT Asp	CAC His 235	GAG Glu	827
GGT Gly	TAT Tyr	GGT Gly	TTT Phe 240	ACC Thr	TCG Ser	AAT Asn	TTA Leu 245	GAA Glu	GTG Val	GAT Asp	TTC Phe	GGC Gly	AAT Asn 250	AAG Lys	AAA Lys	875
TTG Leu	ACG Thr 255	GGT Gly	AAA Lys	TTA Leu	ATA Ile	CGC Arg	AAT Asn 260	AAT Asn	GCG Ala	AGC Ser	CTA Leu	AAT Asn 265	AAT Asn	AAT Asn	ACT Thr	923
AAT Asn 270	AAT Asn	GAC Asp	AAA Lys	CAT His	ACC Thr	ACC Thr 275	CAA Gln	TAC Tyr	TAC Tyr	AGC Ser	CTT Leu 280	GAT Asp	GCA Ala	CAA Gln	ATA Ile	971
ACA Thr 285	GGC Gly	AAC Asn	CGC Arg	TTC Phe	AAC Asn 290	GGC Gly	ACG Thr	GCA Ala	ACG Thr	GCA Ala 295	ACT Thr	GAC Asp	AAA Lys	AAA Lys	GAG Glu 300	1019
AAT Asn	GAA Glu	ACC Thr	AAA Lys	CTA Leu 305	CAT His	CCC Pro	TTT Phe	GTT Val	TCC Ser 310	GAC Asp	TCG Ser	TCT Ser	TCT Ser	TTG Leu 315	AGC Ser	1067
GGC Gly	GGC Gly	TTT Phe	TTC Phe 320	GGC Gly	CCG Pro	CAG Gln	GGT Gly	GAG Glu	GAA Glu	TTG Leu	GGT Gly	TTC Phe	CGC Arg 330	TTT Phe	TTG Leu	1115
AGC Ser	GAC Asp 335	GAT Asp	CAA Gln	AAA Lys	GTT Val	GCC Ala	GTT Val 340	GTC Val	GGC Gly	AGC Ser	GCG Ala	AAA Lys 345	ACC Thr	AAA Lys	GAC Asp	1163

AAA Lys 350	CTG Leu	GAA Glu	AAT Asn	GGC Gly	GCG Ala	GCG Ala 355	GCT Ala	TCA Ser	GGC Gly	AGC Ser	ACA Thr 360	GGT Gly	GCG Ala	GCA Ala	GCA Ala	1211
TCG Ser 365	GGC Gly	GGT Gly	GCG Ala	GCA Ala	GGC Gly 370	ACG Thr	TCG Ser	TCT Ser	GAA Glu	AAC Asn 375	AGT Ser	AAG Lys	CTG Leu	ACC Thr	ACG Thr 380	1259
GTT Val	TTG Leu	GAT Asp	GCG Ala 385	GTT Val	GAA Glu	TTG Leu	ACA Thr	CTA Leu	AAC Asn 390	GAC Asp	AAG Lys	AAA Lys	ATC Ile	AAA Lys 395	AAT Asn	1307
CTC Leu	GAC Asp	AAC Asn 400	TTC Phe	AGC Ser	AAT Asn	GCC Ala	GCC Ala	CAA Gln 405	CTG Leu	GTT Val	GTC Val	GAC Asp	GGC Gly 410	ATT Ile	ATG Met	1355
ATT Ile 5	CCG Pro	CTC Leu 415	CTG Leu	CCC Pro	AAG Lys	GAT Asp	TCC Ser 420	GAA Glu	AGC Ser	GGG Gly	AAC Asn	ACT Thr 425	CAG Gln	GCA Ala	GAT Asp	1403
AAA Lys 430	GGT Gly	AAA Lys	AAC Asn	GGC Gly	GGA Gly	ACA Thr 435	GAA Glu	TTT Phe	ACC Thr	CGC Arg	AAA Lys 440	TTT Phe	GAA Glu	CAC His	ACG Thr	1451
CCG Pro 445	GAA Glu	AGT Ser	GAT Asp	AAA Lys	AAA Lys 450	GAC Asp	GCC Ala	CAA Gln	GCA Ala	GGT Gly 455	ACG Thr	CAG Gln	ACG Thr	AAT Asn	GGG Gly 460	1499
GCG Ala	CAA Gln	ACC Thr	GCT Ala 465	TCA Ser	AAT Asn	ACG Thr	GCA Ala	GGT Gly 470	GAT Asp	ACC Thr	AAT Asn	GGC Gly	AAA Lys 475	ACA Thr	AAA Lys	1547
ACC Thr	TAT Tyr	GAA Glu	GTC Val 480	GAA Glu	GTC Val	TGC Cys	TGT Cys	TCC Ser 485	AAC Asn	CTC Leu	AAT Asn	TAT Tyr	CTG Leu 490	AAA Lys	TAC Tyr	1595
GGA Gly	ATG Met	TTG Leu 495	ACG Thr	CGC Arg	AAA Lys	AAC Asn	AGC Ser 500	AAG Lys	TCC Ser	GCG Ala	ATG Met	CAG Gln 505	GCA Ala	GGA Gly	GGA Gly	1643
AAC Asn 510	AGT Ser	AGT Ser	CAA Gln	GCT Ala	GAT Asp	GCT Ala 515	AAA Lys	ACG Thr	GAA Glu	CAA Gln	GTT Val 520	GAA Glu	CAA Gln	AGT Ser	ATG Met	1691
TTC Phe 525	CTC Leu	CAA Gln	GGC Gly	GAG Glu	CGT Arg 530	ACC Thr	GAT Asp	GAA Glu	AAA Lys	GAG Glu 535	ATT Ile	CCA Pro	ACC Thr	GAC Asp	CAA Gln 540	1739
AAC Asn	GTC Val	GTT Val	TAT Tyr 545	CGG Arg	GGG Gly	TCT Ser	TGG Trp	TAC Tyr	GGG Gly 550	CAT His	ATT Ile	GCC Ala	AAC Asn	GGC Gly 555	ACA Thr	1787
AGC Ser	TGG Trp	AGC Ser	GGC Gly 560	AAT Asn	GCT Ala	TCT Ser	GAT Asp	AAA Lys 565	GAG Glu	GGC Gly	GGC Gly	AAC Asn	AGG Arg 570	GCG Ala	GAA Glu	1835
TTT Phe	ACT Thr	GTG Val 575	AAT Asn	TTT Phe	GCC Ala	GAT Asp	AAA Lys 580	AAA Lys	ATT Ile	ACC Thr	GGC Gly 585	AAG Lys	TTA Leu	ACC Thr	GCT Ala	1883

GAA AAC AGG CAG GCG CAA ACC TTT ACC ATT GAG GGA ATG ATT CAG GGC	1931
Glu Asn Arg Gln Ala Gln Thr Phe Thr Ile Glu Gly Met Ile Gln Gly	
590 595 600	
AAC GGC TTT GAA GGT ACG GCG AAA ACT GCT GAG TCA GGT TTT GAT CTC	1979
Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Glu Ser Gly Phe Asp Leu	
605 610 615 620	
GAT CAA AAA AAT ACC ACC CGC ACG CCT AAG GCA TAT ATC ACA GAT GCC	2027
Asp Gln Lys Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala	
625 630 635	
AAG GTA AAG GGC GGT TTT TAC GGG CCT AAA GCC GAA GAG TTG GGC GGA	2075
Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly	
640 645 650	
TGG TTT GCC TAT CCG GGC GAT AAA CAA ACG GAA AAG GCA ACA GCT ACA	2123
Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Glu Lys Ala Thr Ala Thr	
655 660 665	
TCC AGC GAT GGA AAT TCA GCA AGC AGC GCG ACC GTG GTA TTC GGT GCG	2171
Ser Ser Asp Gly Asn Ser Ala Ser Ser Ala Thr Val Val Phe Gly Ala	
670 675 680	
AAA CGC CAA CAG CCT GTG CAA TAAGCACGGT TGCCGAACAA TCAAGAATAA	2222
Lys Arg Gln Gln Pro Val Gln	
685 690	
GGCTTCAG	2230

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe	
-20 -15 -10 -5	
Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser	
1 5 10	
Val Asp Thr Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser	
15 20 25	
Ser Glu Lys Pro Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala	
30 35 40	
Met Arg Leu Lys Arg Arg Asn Trp Tyr Pro Gly Ala Glu Glu Ser Glu	
45 50 55 60	
Val Lys Leu Asn Glu Ser Asp Trp Glu Ala Thr Gly Leu Pro Thr Lys	
65 70 75	

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Pro	Lys	Glu	Leu	Pro	Lys	Arg	Gln	Lys	Ser	Val	Ile	Glu	Lys	Val	Glu	80	85	90
Thr	Asp	Gly	Asp	Ser	Asp	Ile	Tyr	Ser	Ser	Pro	Tyr	Leu	Thr	Pro	Ser	95	100	105
Asn	His	Gln	Asn	Gly	Ser	Ala	Gly	Asn	Gly	Val	Asn	Gln	Pro	Lys	Asn	110	115	120
Gln	Ala	Thr	Gly	His	Glu	Asn	Phe	Gln	Tyr	Val	Tyr	Ser	Gly	Trp	Phe	125	130	135
Tyr	Lys	His	Ala	Ala	Ser	Glu	Lys	Asp	Phe	Ser	Asn	Lys	Lys	Ile	Lys	145	150	155
Ser	Gly	Asp	Asp	Gly	Tyr	Ile	Phe	Tyr	His	Gly	Glu	Lys	Pro	Ser	Arg	160	165	170
Gln	Leu	Pro	Ala	Ser	Gly	Lys	Val	Ile	Tyr	Lys	Gly	Val	Trp	His	Phe	175	180	185
Val	Thr	Asp	Thr	Lys	Lys	Gly	Gln	Asp	Phe	Arg	Glu	Ile	Ile	Gln	Pro	190	195	200
Ser	Lys	Lys	Gln	Gly	Asp	Arg	Tyr	Ser	Gly	Phe	Ser	Gly	Asp	Gly	Ser	205	210	215
Glu	Glu	Tyr	Ser	Asn	Lys	Asn	Glu	Ser	Thr	Leu	Lys	Asp	Asp	His	Glu	225	230	235
Gly	Tyr	Gly	Phe	Thr	Ser	Asn	Leu	Glu	Val	Asp	Phe	Gly	Asn	Lys	Lys	240	245	250
Leu	Thr	Gly	Lys	Leu	Ile	Arg	Asn	Asn	Ala	Ser	Leu	Asn	Asn	Asn	Thr	255	260	265
Asn	Asn	Asp	Lys	His	Thr	Thr	Gln	Tyr	Tyr	Ser	Leu	Asp	Ala	Gln	Ile	270	275	280
Thr	Gly	Asn	Arg	Phe	Asn	Gly	Thr	Ala	Thr	Ala	Thr	Asp	Lys	Lys	Glu	285	290	295
Asn	Glu	Thr	Lys	Leu	His	Pro	Phe	Val	Ser	Asp	Ser	Ser	Ser	Leu	Ser	305	310	315
Gly	Gly	Phe	Phe	Gly	Pro	Gln	Gly	Glu	Glu	Leu	Gly	Phe	Arg	Phe	Leu	320	325	330
Ser	Asp	Asp	Gln	Lys	Val	Ala	Val	Val	Gly	Ser	Ala	Lys	Thr	Lys	Asp	335	340	345
Lys	Leu	Glu	Asn	Gly	Ala	Ala	Ala	Ser	Gly	Ser	Thr	Gly	Ala	Ala	Ala	350	355	360
Ser	Gly	Gly	Ala	Ala	Gly	Thr	Ser	Ser	Glu	Asn	Ser	Lys	Leu	Thr	Thr	365	370	375
Val	Leu	Asp	Ala	Val	Glu	Leu	Thr	Leu	Asn	Asp	Lys	Lys	Ile	Lys	Asn	385	390	395

Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met
 400 405 410
 Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly Asn Thr Gln Ala Asp
 415 420 425
 Lys Gly Lys Asn Gly Gly Thr Glu Phe Thr Arg Lys Phe Glu His Thr
 430 435 440
 Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln Thr Asn Gly
 445 450 455 460
 Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys Thr Lys
 465 470 475
 Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr
 480 485 490
 Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Gly
 495 500 505
 Asn Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu Gln Ser Met
 510 515 520
 Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Thr Asp Gln
 525 530 535 540
 Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Gly Thr
 545 550 555
 Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn Arg Ala Glu
 560 565 570
 Phe Thr Val Asn Phe Ala Asp Lys Lys Ile Thr Gly Lys Leu Thr Ala
 575 580 585
 Glu Asn Arg Gln Ala Gln Thr Phe Thr Ile Glu Gly Met Ile Gln Gly
 590 595 600
 Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Glu Ser Gly Phe Asp Leu
 605 610 615 620
 Asp Gln Lys Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala
 625 630 635
 Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly
 640 645 650
 Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Glu Lys Ala Thr Ala Thr
 655 660 665
 Ser Ser Asp Gly Asn Ser Ala Ser Ser Ala Thr Val Val Phe Gly Ala
 670 675 680
 Lys Arg Gln Gln Pro Val Gln
 685 690

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1808 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: IM2394

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..60

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 61..1797

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1797

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 61..1035

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1036..1386

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1387..1797

(ix) FEATURE:

- (A) NAME/KEY: misc_binding
- (B) LOCATION: 46..1050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG AAC AAT CCA TTG GTA AAT CAG GCT GCT ATG GTG CTG CCT GTG TTT	48
Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe	
-20 -15 -10 -5	
TTG TTG AGT GCT TGT CTG GGT GGC GGC GGC AGT TTC GAT TTG GAC AGC	96
Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser	
1 5 10	
GTG GAA ACC GTG CAA GAT ATG CAC TCC AAA CCT AAG TAT GAG GAT GAA	144
Val Glu Thr Val Gln Asp Met His Ser Lys Pro Lys Tyr Glu Asp Glu	
15 20 25	
AAA AGC CAG CCT GAA AGC CAA CAG GAT GTA TCG GAA AAC AGC GGC GCG	192
Lys Ser Gln Pro Glu Ser Gln Gln Asp Val Ser Glu Asn Ser Gly Ala	
30 35 40	
GCT TAT GGC TTT GCA GTA AAA CTA CCT CGC CGG AAT GCA CAT TTT AAT	240
Ala Tyr Gly Phe Ala Val Lys Leu Pro Arg Arg Asn Ala His Phe Asn	

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45				50				55				60				
CCT Pro	AAA Lys	TAT Tyr	AAG Lys	GAA Glu 65	AAG Lys	CAC His	AAA Lys	CCA Pro	TTG Leu 70	GGT Gly	TCA Ser	ATG Met	GAT Asp	TGG Trp 75	AAA Lys	288
AAA Lys	CTG Leu	CAA Gln	AGA Arg 80	GGA Gly	GAA Glu	CCA Pro	AAT Asn 85	AGT Ser	TTT Phe	AGT Ser	GAG Glu	AGG Arg	GAT Asp 90	GAA Glu	TTG Leu	336
GAA Glu	AAA Lys	AAA Lys 95	CGG Arg	GGT Gly	AGT Ser	TCT Ser	GAA Glu 100	CTT Leu	ATT Ile	GAA Glu	TCA Ser	AAA Lys 105	TGG Trp	GAA Glu	GAT Asp	384
GGG Gly	CAA Gln 110	AGT Ser	CGT Arg	GTA Val	GTT Val	GGT Gly 115	TAT Tyr	ACA Thr	AAT Asn	TTC Phe	ACT Thr 120	TAT Tyr	GTC Val	CGT Arg	TCG Ser	432
GGA Gly 125	TAT Tyr	GTT Val	TAC Tyr	CTT Leu 130	AAT Asn	AAA Lys	AAT Asn	AAT Asn	ATT Ile 135	GAT Asp	ATT Ile	AAG Lys	AAT Asn	AAT Asn	ATA Ile 140	480
GTT Val	CTT Leu	TTT Phe	GGA Gly 145	CCT Pro	GAC Asp	GGA Gly	TAT Tyr	CTT Leu	TAC Tyr 150	TAT Tyr	AAA Lys	GGG Gly	AAA Lys	GAA Glu 155	CCT Pro	528
TCC Ser	AAG Lys	GAG Glu 160	CTG Leu	CCA Pro	TCG Ser	GAA Glu	AAG Lys	ATA Ile 165	ACT Thr	TAT Tyr	AAA Lys	GGT Gly	ACT Thr 170	TGG Trp	GAT Asp	576
TAT Tyr	GTT Val	ACT Thr 175	GAT Asp	GCT Ala	ATG Met	GAA Glu	AAA Lys 180	CAA Gln	AGG Arg	TTT Phe	GAA Glu	GGA Gly 185	TTG Leu	GGT Gly	AGT Ser	624
GCA Ala 190	GCA Ala	GGA Gly	GGA Gly	GAT Asp	AAA Lys	TCG Ser 195	GGG Gly	GCG Ala	TTG Leu	TCT Ser	GCA Ala 200	TTA Leu	GAA Glu	GAA Glu	GGG Gly	672
GTA Val 205	TTG Leu	CGT Arg	AAT Asn	CAG Gln 210	GCA Ala	GAG Glu	GCA Ala	TCA Ser	TCC Ser	GGT Gly 215	CAT His	ACC Thr	GAT Asp	TTT Phe	GGT Gly 220	720
ATG Met	ACT Thr	AGT Ser	GAG Glu 225	TTT Phe	GAG Glu	GTT Val	GAT Asp	TTT Phe	TCT Ser 230	GAT Asp	AAA Lys	ACA Thr	ATA Ile	AAG Lys 235	GGC Gly	768
ACA Thr	CTT Leu	TAT Tyr 240	CGT Arg	AAC Asn	AAC Asn	CGT Arg	ATT Ile 245	ACT Thr	CAA Gln	AAT Asn	AAT Asn	AGT Ser	GAA Glu 250	AAC Asn	AAA Lys	816
CAA Gln	ATA Ile 255	AAA Lys	ACT Thr	ACG Thr	CGT Arg	TAC Tyr 260	ACC Thr	ATT Ile	CAA Gln	GCA Ala	ACT Thr 265	CTT Leu	CAC His	GGC Gly	AAC Asn	864
CGT Arg 270	TTC Phe	AAA Lys	GGT Gly	AAG Lys	GCG Ala	TTG Leu 275	GCG Ala	GCA Ala	GAT Asp	AAA Lys	GGT Gly 280	GCA Ala	ACA Thr	AAT Asn	GGA Gly	912
AGT Ser	CAT His	CCC Pro	TTT Phe	ATT Ile	TCC Ser	GAC Asp	TCC Ser	GAC Asp	AGT Ser	TTG Leu	GAA Glu	GGC Gly	GGA Gly	TTT Phe	TAC Tyr	960

285				290				295				300				
GGG Gly	CCG Pro	AAA Lys	GGC Gly	GAG Glu 305	GAA Glu	CTT Leu	GCC Ala	GGT Gly	AAA Lys 310	TTC Phe	TTG Leu	AGC Ser	AAC Asn	GAC Asp 315	AAC Asn	1008
AAA Lys	GTT Val	GCA Ala	GCG Ala 320	GTG Val	TTT Phe	GGT Gly	GCG Ala	AAG Lys 325	CAG Gln	AAA Lys	GAT Asp	AAG Lys	AAG Lys 330	GAT Asp	GGG Gly	1056
GAA Glu	AAC Asn	GCG Ala 335	GCA Ala	GGG Gly	CCT Pro	GCA Ala	ACG Thr 340	GAA Glu	ACC Thr	GTG Val	ATA Ile	GAT Asp 345	GCA Ala	TAC Tyr	CGT Arg	1104
ATT Ile	ACC Thr 350	GGC Gly	GAG Glu	GAG Glu	TTT Phe	AAG Lys 355	AAA Lys	GAG Glu	CAA Gln	ATA Ile	GAC Asp 360	AGT Ser	TTT Phe	GGA Gly	GAT Asp	1152
GTG Val 365	AAA Lys	AAG Lys	CTG Leu	CTG Leu	GTT Val 370	GAC Asp	GGA Gly	GTG Val	GAG Glu	CTT Leu 375	TCA Ser	CTG Leu	CTG Leu	CCG Pro	TCT Ser 380	1200
GAG Glu	GGC Gly	AAT Asn	AAG Lys	GCG Ala 385	GCA Ala	TTT Phe	CAG Gln	CAC His	GAG Glu 390	ATT Ile	GAG Glu	CAA Gln	AAC Asn	GGC Gly 395	GTG Val	1248
AAG Lys	GCA Ala	ACG Thr	GTG Val 400	TGT Cys	TGT Cys	TCC Ser	AAC Asn	TTG Leu 405	GAT Asp	TAC Tyr	ATG Met	AGT Ser	TTT Phe 410	GGG Gly	AAG Lys	1296
CTG Leu	TCA Ser	AAA Lys 415	GAA Glu	AAT Asn	AAA Lys	GAC Asp	GAT Asp 420	ATG Met	TTC Phe	CTG Leu	CAA Gln	GGT Gly 425	GTC Val	CGC Arg	ACT Thr	1344
CCA Pro	GTA Val 430	TCC Ser	GAT Asp	GTG Val	GCG Ala	GCA Ala 435	AGG Arg	ACG Thr	GAG Glu	GCA Ala	AAC Asn 440	GCC Ala	AAA Lys	TAT Tyr	CGC Arg	1392
GGT Gly 445	ACT Thr	TGG Trp	TAC Tyr	GGA Gly	TAT Tyr 450	ATT Ile	GCC Ala	AAC Asn	GGC Gly	ACA Thr 455	AGC Ser	TGG Trp	AGC Ser	GGC Gly	GAA Glu 460	1440
GCC Ala	TCC Ser	AAT Asn	CAG Gln	GAA Glu 465	GGT Gly	GGT Gly	AAT Asn	AGG Arg	GCA Ala 470	GAG Glu	TTT Phe	GAC Asp	GTG Val	GAT Asp 475	TTT Phe	1488
TCC Ser	ACT Thr	AAA Lys	AAA Lys 480	ATC Ile	AGT Ser	GGC Gly	ACA Thr	CTG Leu 485	ACG Thr	GCA Ala	AAA Lys	GAC Asp	CGT Arg 490	ACG Thr	TCT Ser	1536
CCT Pro	GCG Ala	TTT Phe 495	ACT Thr	ATT Ile	ACT Thr	GCC Ala	ATG Met 500	ATT Ile	AAG Lys	GAC Asp	AAC Asn	GGT Gly 505	TTT Phe	TCA Ser	GGT Gly	1584
GTG Val	GCG Ala 510	AAA Lys	ACC Thr	GGT Gly	GAA Glu	AAC Asn 515	GGC Gly	TTT Phe	GCG Ala	CTG Leu	GAT Asp 520	CCG Pro	CAA Gln	AAT Asn	ACC Thr	1632
GGA Gly	AAT Asn	TCC Ser	CAC His	TAT Tyr	ACG Thr	CAT His	ATT Ile	GAA Glu	GCC Ala	ACT Thr	GTA Val	TCC Ser	GGC Gly	GGT Gly	TTC Phe	1680

525	530	535	540	
TAC GGC AAA AAC GCC ATC GAG ATG GGC GGA TCG TTC TCA TTT CCG GGA				1728
Tyr Gly Lys Asn Ala Ile Glu Met Gly Gly Ser Phe Ser Phe Pro Gly	545	550	555	
AAT GCA CCA GAG GGA AAA CAA GAA AAA GCA TCG GTG GTA TTC GGT GCG				1776
Asn Ala Pro Glu Gly Lys Gln Glu Lys Ala Ser Val Val Phe Gly Ala	560	565	570	
AAA CGC CAA CAG CTT GTG CAA TAAGCACGGC T				1808
Lys Arg Gln Gln Leu Val Gln	575			

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 599 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe	-20	-15	-10	-5
Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser	1	5	10	
Val Glu Thr Val Gln Asp Met His Ser Lys Pro Lys Tyr Glu Asp Glu	15	20	25	
Lys Ser Gln Pro Glu Ser Gln Gln Asp Val Ser Glu Asn Ser Gly Ala	30	35	40	
Ala Tyr Gly Phe Ala Val Lys Leu Pro Arg Arg Asn Ala His Phe Asn	45	50	55	60
Pro Lys Tyr Lys Glu Lys His Lys Pro Leu Gly Ser Met Asp Trp Lys	65	70	75	
Lys Leu Gln Arg Gly Glu Pro Asn Ser Phe Ser Glu Arg Asp Glu Leu	80	85	90	
Glu Lys Lys Arg Gly Ser Ser Glu Leu Ile Glu Ser Lys Trp Glu Asp	95	100	105	
Gly Gln Ser Arg Val Val Gly Tyr Thr Asn Phe Thr Tyr Val Arg Ser	110	115	120	
Gly Tyr Val Tyr Leu Asn Lys Asn Asn Ile Asp Ile Lys Asn Asn Ile	125	130	135	140
Val Leu Phe Gly Pro Asp Gly Tyr Leu Tyr Tyr Lys Gly Lys Glu Pro	145	150	155	
Ser Lys Glu Leu Pro Ser Glu Lys Ile Thr Tyr Lys Gly Thr Trp Asp				

160

165

170

Tyr	Val	Thr	Asp	Ala	Met	Glu	Lys	Gln	Arg	Phe	Glu	Gly	Leu	Gly	Ser
		175					180					185			
Ala	Ala	Gly	Gly	Asp	Lys	Ser	Gly	Ala	Leu	Ser	Ala	Leu	Glu	Glu	Gly
	190					195					200				
Val	Leu	Arg	Asn	Gln	Ala	Glu	Ala	Ser	Ser	Gly	His	Thr	Asp	Phe	Gly
205				210						215					220
Met	Thr	Ser	Glu	Phe	Glu	Val	Asp	Phe	Ser	Asp	Lys	Thr	Ile	Lys	Gly
				225					230					235	
Thr	Leu	Tyr	Arg	Asn	Asn	Arg	Ile	Thr	Gln	Asn	Asn	Ser	Glu	Asn	Lys
			240				245						250		
Gln	Ile	Lys	Thr	Thr	Arg	Tyr	Thr	Ile	Gln	Ala	Thr	Leu	His	Gly	Asn
		255					260					265			
Arg	Phe	Lys	Gly	Lys	Ala	Leu	Ala	Ala	Asp	Lys	Gly	Ala	Thr	Asn	Gly
	270					275					280				
Ser	His	Pro	Phe	Ile	Ser	Asp	Ser	Asp	Ser	Leu	Glu	Gly	Gly	Phe	Tyr
285				290						295					300
Gly	Pro	Lys	Gly	Glu	Glu	Leu	Ala	Gly	Lys	Phe	Leu	Ser	Asn	Asp	Asn
				305					310					315	
Lys	Val	Ala	Ala	Val	Phe	Gly	Ala	Lys	Gln	Lys	Asp	Lys	Lys	Asp	Gly
			320					325					330		
Glu	Asn	Ala	Ala	Gly	Pro	Ala	Thr	Glu	Thr	Val	Ile	Asp	Ala	Tyr	Arg
		335					340					345			
Ile	Thr	Gly	Glu	Glu	Phe	Lys	Lys	Glu	Gln	Ile	Asp	Ser	Phe	Gly	Asp
	350					355					360				
Val	Lys	Lys	Leu	Leu	Val	Asp	Gly	Val	Glu	Leu	Ser	Leu	Leu	Pro	Ser
365					370					375					380
Glu	Gly	Asn	Lys	Ala	Ala	Phe	Gln	His	Glu	Ile	Glu	Gln	Asn	Gly	Val
				385					390					395	
Lys	Ala	Thr	Val	Cys	Cys	Ser	Asn	Leu	Asp	Tyr	Met	Ser	Phe	Gly	Lys
			400					405					410		
Leu	Ser	Lys	Glu	Asn	Lys	Asp	Asp	Met	Phe	Leu	Gln	Gly	Val	Arg	Thr
		415					420					425			
Pro	Val	Ser	Asp	Val	Ala	Ala	Arg	Thr	Glu	Ala	Asn	Ala	Lys	Tyr	Arg
						435					440				
Gly	Thr	Trp	Tyr	Gly	Tyr	Ile	Ala	Asn	Gly	Thr	Ser	Trp	Ser	Gly	Glu
445					450					455					460
Ala	Ser	Asn	Gln	Glu	Gly	Gly	Asn	Arg	Ala	Glu	Phe	Asp	Val	Asp	Phe
				465					470					475	
Ser	Thr	Lys	Lys	Ile	Ser	Gly	Thr	Leu	Thr	Ala	Lys	Asp	Arg	Thr	Ser

480

485

490

Pro Ala Phe Thr Ile Thr Ala Met Ile Lys Asp Asn Gly Phe Ser Gly
495 500 505

Val Ala Lys Thr Gly Glu Asn Gly Phe Ala Leu Asp Pro Gln Asn Thr
510 515 520

Gly Asn Ser His Tyr Thr His Ile Glu Ala Thr Val Ser Gly Gly Phe
525 530 535 540

Tyr Gly Lys Asn Ala Ile Glu Met Gly Gly Ser Phe Ser Phe Pro Gly
545 550 555

Asn Ala Pro Glu Gly Lys Gln Glu Lys Ala Ser Val Val Phe Gly Ala
560 565 570

Lys Arg Gln Gln Leu Val Gln
575

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2255 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
(B) STRAIN: M978

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
(B) LOCATION: 1..2115

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..2115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGT CTG GGT GGC GGC GGC ACG TTC GAT CTT GAT TCT GTC GAT ACC GAA 48
Cys Leu Gly Gly Gly Gly Thr Phe Asp Leu Asp Ser Val Asp Thr Glu
1 5 10 15

GCC CCG CGT CCC GCC CCA AAA TAT CAA GAT GTT TCT TCC GAA AAA CCG 96
Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser Ser Glu Lys Pro
20 25 30

CAA GCC CAA AAA GAC CAA GGC GGA TAC GGT TTT GCA ATG CGC CTC AAG 144
Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Leu Lys
35 40 45

CGG CGG AAT TGG CAT CCG CAG GCA AAT CCT AAA GAA GAT GAG ATA AAA 192
Arg Arg Asn Trp His Pro Gln Ala Asn Pro Lys Glu Asp Glu Ile Lys
50 55 60

101

CTT Leu 65	TCT Ser	GAA Glu	AAT Asn	GAT Asp	TGG Trp 70	GAG Glu	GCG Ala	ACA Thr	GGA Gly	TTG Leu 75	CCA Pro	GGC Gly	AAT Asn	CCC Pro	AAA Lys 80	240
AAC Asn	TTA Leu	CCT Pro	GAG Glu	CGA Arg 85	CAG Gln	AAA Lys	TCG Ser	GTT Val	ATT Ile 90	GAA Glu	AAA Lys	GTA Val	AAA Lys	ACA Thr 95	GGC Gly	288
AGC Ser	GAC Asp	AGC Ser	AAT Asn 100	ATT Ile	TAT Tyr	TCT Ser	TCC Ser	CCC Pro 105	TAT Tyr	CTC Leu	ACG Thr	CAA Gln	TCA Ser 110	AAC Asn	CAT His	336
CAA Gln	AAC Asn	GGC Gly 115	AGT Ser	GCA Ala	AAC Asn	CAA Gln	CCA Pro 120	AAA Lys	AAT Asn	GAA Glu	GTA Val	AAA Lys 125	GAT Asp	TAT Tyr	AAA Lys	384
GAG Glu 130	TTC Phe	AAA Lys	TAT Tyr	GTT Val	TAT Tyr	TCC Ser 135	GGT Gly	TGG Trp	TTT Phe	TAC Tyr	AAA Lys 140	CAC His	GCT Ala	AAA Lys	CTC Leu	432
GAA Glu 145	ATC Ile	ATA Ile	AAA Lys	GAA Glu	AAC Asn 150	AAC Asn	TTA Leu	ATT Ile	AAG Lys	GGT Gly 155	GCA Ala	AAG Lys	AGC Ser	GGC Gly	GAC Asp 160	480
GAC Asp	GGT Gly	TAT Tyr	ATC Ile	TTT Phe 165	TAT Tyr	CAC His	GGT Gly	GAA Glu	AAA Lys 170	CCT Pro	TCC Ser	CGA Arg	CAA Gln	CTT Leu 175	CCC Pro	528
GTT Val	TCT Ser	GGA Gly	GAA Glu	GTT Val 180	ACC Thr	TAC Tyr	AAA Lys	GGC Gly 185	GTA Val	TGG Trp	CAT His	TTT Phe	GTA Val 190	ACC Thr	GAT Asp	576
ACG Thr	AAA Lys	CAG Gln 195	GGA Gly	CAA Gln	AAA Lys	TTT Phe	AAC Asn 200	GAT Asp	ATT Ile	CTT Leu	GGA Gly	ACC Thr 205	TCA Ser	AAA Lys	AAA Lys	624
CAA Gln 210	GGC Gly	GAC Asp	AGG Arg	TAT Tyr	AGC Ser	GGA Gly 215	TTT Phe	CCG Pro	GGT Gly	GAT Asp	GAC Asp 220	GGC Gly	GAA Glu	GAA Glu	TAT Tyr	672
TCC Ser 225	AAT Asn	AAA Lys	AAT Asn	GAA Glu	GCG Ala 230	ACT Thr	TTA Leu	CAA Gln	GGC Gly	AGT Ser 235	CAA Gln	GAG Glu	GGT Gly	TAT Tyr	GGT Gly 240	720
TTT Phe	ACC Thr	TCA Ser	AAT Asn	TTA Leu 245	AAA Lys	GTG Val	GAT Asp	TTC Phe	AAT Asn 250	AAG Lys	AAA Lys	AAA Lys	TTG Leu	ACG Thr 255	GGT Gly	768
GAA Glu	TTG Leu	ATA Ile	CGC Arg 260	AAT Asn	AAT Asn	AGA Arg	GTT Val	ACA Thr 265	AAC Asn	GCT Ala	ACT Thr	GCT Ala	AAC Asn 270	GAT Asp	AAA Lys	816
TAC Tyr	ACC Thr	ACC Thr 275	CAA Gln	TAT Tyr	TAC Tyr	AGC Ser	CTT Leu 280	GAG Glu	GCT Ala	CAA Gln	GTA Val	ACA Thr 285	GGC Gly	AAC Asn	CGC Arg	864
TTC Phe 290	AAC Asn	GGC Gly	AAG Lys	GCA Ala	ACG Thr	GCA Ala 295	ACC Thr	GAC Asp	AAA Lys	CCT Pro	GGC Gly 300	ACT Thr	GGA Gly	GAA Glu	ACC Thr	912

AAA Lys 305	CAA Gln	CAT His	CCC Pro	TTT Phe 310	GTT Val	TCC Ser	GAC Asp	TCG Ser	TCT Ser 315	TCT Ser	TTG Leu	AGC Ser	GGC Gly	GGC Gly	TTT Phe 320	960
TTC Phe	GGC Gly	CCG Pro	AAG Lys 325	GGT Gly	GAG Glu	GAA Glu	TTG Leu	GGT Gly	TTC Phe 330	CGC Arg	TTT Phe	TTG Leu	AGC Ser	AAC Asn 335	GAT Asp	1008
CAA Gln	AAA Lys	GTT Val 340	GCC Ala	GTT Val	GTC Val	GGC Gly	AGC Ser	GCG Ala 345	AAA Lys	ACC Thr	CAA Gln	GAC Asp	AAA Lys 350	GCC Ala	GCA Ala	1056
AAT Asn	GGC Gly 355	AAT Asn	ACT Thr	GCG Ala	GCG Ala	GCT Ala 360	TCA Ser	GGC Gly	GGC Gly	ACA Thr	GAT Asp 365	GCG Ala	GCA Ala	GCA Ala	TCA Ser	1104
AAC Asn 370	GGT Gly	GCG Ala	GCA Ala	GGC Gly	ACG Thr	TCG Ser 375	TCT Ser	GAA Glu	AAC Asn	AGT Ser	AAG Lys 380	CTG Leu	ACC Thr	ACG Thr	GTT Val	1152
TTG Leu 385	GAT Asp	GCG Ala	GTT Val	GAA Glu	TTG Leu 390	ACA Thr	CTA Leu	AAC Asn	GAC Asp 395	AAG Lys	AAA Lys	ATC Ile	AAA Lys	AAT Asn	CTC Leu 400	1200
GAC Asp	AAC Asn	TTC Phe	AGC Ser 405	AAT Asn	GCC Ala	GCC Ala	CAA Gln	CTG Leu	GTT Val 410	GTC Val	GAC Asp	GGC Gly	ATT Ile	ATG Met 415	ATT Ile	1248
CCG Pro	CTC Leu	CTG Leu 420	CCC Pro	GAG Glu	ACT Thr	TCC Ser	GAA Glu	AGT Ser 425	GGG Gly	AGC Ser	AAT Asn	CAG Gln	GCA Ala 430	GAT Asp	AAA Lys	1296
GGT Gly	AAA Lys 435	AAA Lys	GGT Gly	AAA Lys	AAC Asn	GGT Gly 440	AAA Lys	AAC Asn	GGC Gly	GGA Gly	ACA Thr	GAC Asp 445	TTT Phe	ACC Thr	TAC Tyr	1344
AAA Lys 450	ACA Thr	ACC Thr	TAC Tyr	ACG Thr	CCG Pro	AAA Lys 455	AAC Asn	GAT Asp	GAC Asp	AAA Lys	GAT Asp 460	ACC Thr	AAA Lys	GCC Ala	CAA Gln	1392
ACA Thr 465	GGT Gly	GCG Ala	GCA Ala	GGC Gly	TCT Ser 470	AGC Ser	GGC Gly	GCA Ala	CAA Gln	ACC Thr 475	GAT Asp	TTG Leu	GGT Gly	AAG Lys	GCG Ala 480	1440
GAC Asp	GTT Val	AAC Asn	GGC Gly 485	GGT Gly	AAG Lys	GCA Ala	GAA Glu	ACA Thr	AAA Lys 490	ACC Thr	TAT Tyr	GAA Glu	GTC Val	GAA Glu 495	GTC Val	1488
TGC Cys	TGT Cys	TCC Ser 500	AAC Asn	CTC Leu	AAT Asn	TAT Tyr	CTG Leu	AAA Lys 505	TAC Tyr	GGA Gly	ATG Met	TTG Leu	ACG Thr 510	CGT Arg	AAA Lys	1536
AAC Asn 515	AGC Ser	AAG Lys	TCC Ser	GCG Ala	ATG Met	CAG Gln	GCA Ala 520	GGA Gly	GGA Gly	AAC Asn	AGT Ser 525	AGT Ser	CAA Gln	GCT Ala	GAT Asp	1584
GCT Ala 530	AAA Lys	ACG Thr	GAA Glu	CAA Gln	GTT Val	GAA Glu 535	CAA Gln	AGT Ser	ATG Met	TTC Phe	CTC Leu 540	CAA Gln	GGC Gly	GAG Glu	CGT Arg	1632

ACC Thr 545	GAT Asp	GAA Glu	AAA Lys	GAG Glu	ATT Ile 550	CCA Pro	AAC Asn	GAC Asp	CAA Gln	AAC Asn 555	GTC Val	GTT Val	TAT Tyr	CGG Arg	GGG Gly 560	1680														
TCT Ser	TGG Trp	TAC Tyr	GGG Gly	CAT His 565	ATT Ile	GCC Ala	AGC Ser	AGC Ser	ACA Thr 570	AGC Ser	TGG Trp	AGC Ser	GGC Gly	AAT Asn 575	GCT Ala	1728														
TCC Ser	AAT Asn	GCA Ala	ACG Thr 580	AGT Ser	GGC Gly	AAC Asn	AGG Arg	GCG Ala 585	GAA Glu	TTT Phe	ACT Thr	GTG Val	AAT Asn 590	TTC Phe	GAT Asp	1776														
ACG Thr	AAA Lys	AAA Lys 595	ATT Ile	AAC Asn	GGC Gly	ACG Thr	TTA Leu 600	ACC Thr	GCT Ala	GAA Glu	AAC Asn	AGG Arg 605	CAG Gln	GAG Glu	GCA Ala	1824														
ACC Thr 610	TTT Phe	ACC Thr	ATT Ile	GAT Asp	GGT Gly	AAG Lys 615	ATT Ile	GAG Glu	GGC Gly	AAC Asn	GGT Gly 620	TTT Phe	TCC Ser	GGT Gly	ACG Thr	1872														
GCA Ala 625	AAA Lys	ACT Thr	GCT Ala	GAC Asp	TTA Leu 630	GGT Gly	TTT Phe	GAT Asp	CTC Leu	GAT Asp 635	CAA Gln	AGC Ser	AAT Asn	ACC Thr	ACC Thr 640	1920														
GGC Gly	ACG Thr	CCT Pro	AAG Lys	GCA Ala 645	TAT Tyr	ATC Ile	ACA Thr	GAT Asp	GCC Ala 650	AAG Lys	GTG Val	CAG Gln	GGC Gly	GGT Gly 655	TTT Phe	1968														
TAC Tyr	GGG Gly	CCT Pro	AAA Lys 660	GCC Ala	GAA Glu	GAG Glu	TTG Leu	GGC Gly 665	GGA Gly	TGG Trp	TTT Phe	GCC Ala	TAT Tyr 670	CCG Pro	GGC Gly	2016														
GAT Asp	AAA Lys	CAA Gln 675	ACG Thr	GAA Glu	AAG Lys	GCA Ala	ACG Thr 680	GTT Val	GCA Ala	TCC Ser	GGC Gly 685	GAT Asp	GGA Gly	AAT Asn	TCA Ser	2064														
GCA Ala 690	AGC Ser	AGC Ser	GCG Ala	ACC Thr	GTG Val	GTA Val 695	TTC Phe	GGT Gly	GCG Ala	AAA Lys	CGC Arg 700	CAA Gln	CAG Gln	CCT Pro	GTG Val	2112														
CAA Gln 705	TAACTAAATG AAGTTGTCTG GGTGGCGGCG GCACGTTCGA TCTTGATTCT														2165															
GTCGATACCG AAGCCCCGCG TCCCGCCCCA AAATATCAAG ATGTTTCTTC CGAAAAACCG																2225														
CAAGCCCAAA AAGACCAAGG CGGATACGGT																2255														

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Cys 1	Leu	Gly	Gly	Gly 5	Gly	Thr	Phe	Asp	Leu 10	Asp	Ser	Val	Asp	Thr 15	Glu
Ala	Pro	Arg	Pro 20	Ala	Pro	Lys	Tyr	Gln 25	Asp	Val	Ser	Ser	Glu 30	Lys	Pro
Gln	Ala	Gln 35	Lys	Asp	Gln	Gly	Gly 40	Tyr	Gly	Phe	Ala	Met 45	Arg	Leu	Lys
Arg 50	Arg	Asn	Trp	His	Pro	Gln 55	Ala	Asn	Pro	Lys	Glu 60	Asp	Glu	Ile	Lys
Leu 65	Ser	Glu	Asn	Asp	Trp 70	Glu	Ala	Thr	Gly	Leu 75	Pro	Gly	Asn	Pro	Lys 80
Asn	Leu	Pro	Glu	Arg 85	Gln	Lys	Ser	Val	Ile 90	Glu	Lys	Val	Lys	Thr 95	Gly
Ser	Asp	Ser	Asn 100	Ile	Tyr	Ser	Ser	Pro 105	Tyr	Leu	Thr	Gln	Ser 110	Asn	His
Gln	Asn 115	Gly	Ser	Ala	Asn	Gln	Pro 120	Lys	Asn	Glu	Val	Lys 125	Asp	Tyr	Lys
Glu 130	Phe	Lys	Tyr	Val	Tyr	Ser 135	Gly	Trp	Phe	Tyr	Lys 140	His	Ala	Lys	Leu
Glu 145	Ile	Ile	Lys	Glu	Asn 150	Asn	Leu	Ile	Lys	Gly 155	Ala	Lys	Ser	Gly	Asp 160
Asp	Gly	Tyr	Ile	Phe 165	Tyr	His	Gly	Glu	Lys 170	Pro	Ser	Arg	Gln	Leu 175	Pro
Val	Ser	Gly	Glu 180	Val	Thr	Tyr	Lys	Gly 185	Val	Trp	His	Phe	Val 190	Thr	Asp
Thr	Lys 195	Gln	Gly	Gln	Lys	Phe	Asn 200	Asp	Ile	Leu	Gly	Thr 205	Ser	Lys	Lys
Gln 210	Gly	Asp	Arg	Tyr	Ser	Gly 215	Phe	Pro	Gly	Asp	Asp 220	Gly	Glu	Glu	Tyr
Ser 225	Asn	Lys	Asn	Glu	Ala 230	Thr	Leu	Gln	Gly	Ser 235	Gln	Glu	Gly	Tyr	Gly 240
Phe	Thr	Ser	Asn 245	Leu	Lys	Val	Asp	Phe	Asn 250	Lys	Lys	Lys	Leu	Thr 255	Gly
Glu	Leu	Ile 260	Arg	Asn	Asn	Arg	Val 265	Thr	Asn	Ala	Thr	Ala 270	Asn	Asp	Lys
Tyr	Thr 275	Thr	Gln	Tyr	Tyr	Ser	Leu 280	Glu	Ala	Gln	Val	Thr 285	Gly	Asn	Arg
Phe	Asn 290	Gly	Lys	Ala	Thr	Ala 295	Thr	Asp	Lys	Pro	Gly 300	Thr	Gly	Glu	Thr
Lys 305	Gln	His	Pro	Phe	Val 310	Ser	Asp	Ser	Ser	Ser 315	Leu	Ser	Gly	Gly	Phe 320

105

Phe	Gly	Pro	Lys	Gly	Glu	Glu	Leu	Gly	Phe	Arg	Phe	Leu	Ser	Asn	Asp	325	330	335
Gln	Lys	Val	Ala	Val	Val	Gly	Ser	Ala	Lys	Thr	Gln	Asp	Lys	Ala	Ala	340	345	350
Asn	Gly	Asn	Thr	Ala	Ala	Ala	Ser	Gly	Gly	Thr	Asp	Ala	Ala	Ala	Ser	355	360	365
Asn	Gly	Ala	Ala	Gly	Thr	Ser	Ser	Glu	Asn	Ser	Lys	Leu	Thr	Thr	Val	370	375	380
Leu	Asp	Ala	Val	Glu	Leu	Thr	Leu	Asn	Asp	Lys	Lys	Ile	Lys	Asn	Leu	385	390	395
Asp	Asn	Phe	Ser	Asn	Ala	Ala	Gln	Leu	Val	Val	Asp	Gly	Ile	Met	Ile	405	410	415
Pro	Leu	Leu	Pro	Glu	Thr	Ser	Glu	Ser	Gly	Ser	Asn	Gln	Ala	Asp	Lys	420	425	430
Gly	Lys	Lys	Gly	Lys	Asn	Gly	Lys	Asn	Gly	Gly	Thr	Asp	Phe	Thr	Tyr	435	440	445
Lys	Thr	Thr	Tyr	Thr	Pro	Lys	Asn	Asp	Asp	Lys	Asp	Thr	Lys	Ala	Gln	450	455	460
Thr	Gly	Ala	Ala	Gly	Ser	Ser	Gly	Ala	Gln	Thr	Asp	Leu	Gly	Lys	Ala	465	470	475
Asp	Val	Asn	Gly	Gly	Lys	Ala	Glu	Thr	Lys	Thr	Tyr	Glu	Val	Glu	Val	485	490	495
Cys	Cys	Ser	Asn	Leu	Asn	Tyr	Leu	Lys	Tyr	Gly	Met	Leu	Thr	Arg	Lys	500	505	510
Asn	Ser	Lys	Ser	Ala	Met	Gln	Ala	Gly	Gly	Asn	Ser	Ser	Gln	Ala	Asp	515	520	525
Ala	Lys	Thr	Glu	Gln	Val	Glu	Gln	Ser	Met	Phe	Leu	Gln	Gly	Glu	Arg	530	535	540
Thr	Asp	Glu	Lys	Glu	Ile	Pro	Asn	Asp	Gln	Asn	Val	Val	Tyr	Arg	Gly	545	550	555
Ser	Trp	Tyr	Gly	His	Ile	Ala	Ser	Ser	Thr	Ser	Trp	Ser	Gly	Asn	Ala	565	570	575
Ser	Asn	Ala	Thr	Ser	Gly	Asn	Arg	Ala	Glu	Phe	Thr	Val	Asn	Phe	Asp	580	585	590
Thr	Lys	Lys	Ile	Asn	Gly	Thr	Leu	Thr	Ala	Glu	Asn	Arg	Gln	Glu	Ala	595	600	605
Thr	Phe	Thr	Ile	Asp	Gly	Lys	Ile	Glu	Gly	Asn	Gly	Phe	Ser	Gly	Thr	610	615	620
Ala	Lys	Thr	Ala	Asp	Leu	Gly	Phe	Asp	Leu	Asp	Gln	Ser	Asn	Thr	Thr	625	630	635

Gly Thr Pro Lys Ala Tyr Ile Thr Asp Ala Lys Val Gln Gly Gly Phe
645 650 655

Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly
660 665 670

Asp Lys Gln Thr Glu Lys Ala Thr Val Ala Ser Gly Asp Gly Asn Ser
675 680 685

Ala Ser Ser Ala Thr Val Val Phe Gly Ala Lys Arg Gln Gln Pro Val
690 695 700

Gln
705

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2114 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
(B) STRAIN: 6940

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
(B) LOCATION: 1..2079

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..2079

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGT	TTG	GGT	GGC	GGC	GGC	ACG	TTC	GAT	CTT	GAT	TCT	GTC	GAT	ACC	GAA	48
Cys	Leu	Gly	Gly	Gly	Gly	Thr	Phe	Asp	Leu	Asp	Ser	Val	Asp	Thr	Glu	
1				5					10					15		
GCC	CCG	CGT	CCC	GAC	CCA	AAG	TAT	CAA	GAT	GTT	TCT	TCC	GAA	AAA	CCG	96
Ala	Pro	Arg	Pro	Asp	Pro	Lys	Tyr	Gln	Asp	Val	Ser	Ser	Glu	Lys	Pro	
			20					25					30			
CAA	GCC	CAA	AAA	GAC	CAA	GGC	GGA	TAC	GGT	TTT	GCG	ATG	AGG	TTG	AAA	144
Gln	Ala	Gln	Lys	Asp	Gln	Gly	Gly	Tyr	Gly	Phe	Ala	Met	Arg	Leu	Lys	
			35				40					45				
CGG	AGG	AAT	TGG	TAT	TCC	GCA	GCA	AAA	GAA	GAC	GAG	GTT	AAA	CTG	AAC	192
Arg	Arg	Asn	Trp	Tyr	Ser	Ala	Ala	Lys	Glu	Asp	Glu	Val	Lys	Leu	Asn	
			50				55				60					
GAG	AGT	GAT	TGG	GAG	ACG	ACA	GGA	TTG	CCG	ACA	GAA	CCC	AAG	AAA	CTG	240
Glu	Ser	Asp	Trp	Glu	Thr	Thr	Gly	Leu	Pro	Thr	Glu	Pro	Lys	Lys	Leu	
65					70				75						80	

CCA	TTA	AAA	CAA	GAA	TCC	GTC	ATT	TCA	AAA	GTA	CAA	GCA	AAC	AAT	GGC	288
Pro	Leu	Lys	Gln	Glu	Ser	Val	Ile	Ser	Lys	Val	Gln	Ala	Asn	Asn	Gly	
				85					90					95		
GAC	AAC	AAT	ATT	TAC	ACT	TCC	CCC	TAT	CTC	ACG	CAA	TCA	AAC	CAT	CAA	336
Asp	Asn	Asn	Ile	Tyr	Thr	Ser	Pro	Tyr	Leu	Thr	Gln	Ser	Asn	His	Gln	
			100					105					110			
AAT	AGC	AGC	ATT	AAT	GGC	GGT	GCA	AAC	CTG	CCA	AAA	AAC	GAA	GTA	ACA	384
Asn	Ser	Ser	Ile	Asn	Gly	Gly	Ala	Asn	Leu	Pro	Lys	Asn	Glu	Val	Thr	
			115				120					125				
AAT	TAT	AAA	GAT	TTC	AAA	TAT	GTT	TAT	TCC	GGC	TGG	TTT	TAT	AAA	CAT	432
Asn	Tyr	Lys	Asp	Phe	Lys	Tyr	Val	Tyr	Ser	Gly	Trp	Phe	Tyr	Lys	His	
	130					135					140					
GCT	AAA	AAC	GAA	ATC	ATA	AGA	GAA	AAC	AGC	TCA	ATT	AAG	GGT	GCA	AAG	480
Ala	Lys	Asn	Glu	Ile	Ile	Arg	Glu	Asn	Ser	Ser	Ile	Lys	Gly	Ala	Lys	
145					150					155					160	
AAC	GGC	GAC	GAC	GGC	TAT	ATC	TTT	TAT	CAC	GGC	AAA	GAA	CCT	TCC	CGA	528
Asn	Gly	Asp	Asp	Gly	Tyr	Ile	Phe	Tyr	His	Gly	Lys	Glu	Pro	Ser	Arg	
				165					170					175		
CAA	CTT	CCC	GCT	TCT	GGA	ACA	GTT	ACC	TAT	AAA	GGT	GTG	TGG	CAT	TTT	576
Gln	Leu	Pro	Ala	Ser	Gly	Thr	Val	Thr	Tyr	Lys	Gly	Val	Trp	His	Phe	
			180					185					190			
GCG	ACC	GAT	GTC	AAA	AAA	TCC	CAA	AAT	TTT	CGC	GAT	ATT	ATC	CAG	CCT	624
Ala	Thr	Asp	Val	Lys	Lys	Ser	Gln	Asn	Phe	Arg	Asp	Ile	Ile	Gln	Pro	
		195					200					205				
TCG	AAA	AAA	CAA	GGC	GAC	AGG	TAT	AGC	GGA	TTT	TCG	GGC	GAT	GAT	GAT	672
Ser	Lys	Lys	Gln	Gly	Asp	Arg	Tyr	Ser	Gly	Phe	Ser	Gly	Asp	Asp	Asp	
	210					215					220					
GAA	CAA	TAT	TCT	AAT	AAA	AAC	GAA	TCC	ATG	CTG	AAA	GAT	GGT	CAA	GAG	720
Glu	Gln	Tyr	Ser	Asn	Lys	Asn	Glu	Ser	Met	Leu	Lys	Asp	Gly	Gln	Glu	
225					230					235					240	
GGT	TAT	GGT	TTT	ACC	TCG	AAT	TTA	GAA	GTG	GAT	TTC	GGC	AGT	AAA	AAA	768
Gly	Tyr	Gly	Phe	Thr	Ser	Asn	Leu	Glu	Val	Asp	Phe	Gly	Ser	Lys	Lys	
				245					250					255		
TTG	ACG	GGT	AAA	TTA	ATA	CGC	AAT	AAT	AGA	GTT	ACA	AAC	GCT	CCT	ACT	816
Leu	Thr	Gly	Lys	Leu	Ile	Arg	Asn	Asn	Arg	Val	Thr	Asn	Ala	Pro	Thr	
			260					265					270			
AAC	GAT	AAA	TAC	ACC	ACC	CAA	TAC	TAC	AGC	CTT	GAT	GCC	CAA	ATA	ACA	864
Asn	Asp	Lys	Tyr	Thr	Thr	Gln	Tyr	Tyr	Ser	Leu	Asp	Ala	Gln	Ile	Thr	
		275					280					285				
GGC	AAC	CGC	TTC	AAC	GGT	AAG	GCG	ATA	CGG	ACC	GAC	AAA	CCC	GAC	ACT	912
Gly	Asn	Arg	Phe	Asn	Gly	Lys	Ala	Ile	Arg	Thr	Asp	Lys	Pro	Asp	Thr	
	290					295					300					
GGA	GGA	ACC	AAA	CTA	CAT	CCC	TTT	GTT	TCC	GAC	TCG	TCT	TCT	TTG	AGC	960
Gly	Gly	Thr	Lys	Leu	His	Pro	Phe	Val	Ser	Asp	Ser	Ser	Ser	Leu	Ser	
305					310					315					320	

GGC Gly	GGC Gly	TTT Phe	TTC Phe	GGT Gly 325	CCG Pro	AAG Lys	GGT Gly	GAG Glu	GAA Glu 330	TTG Leu	GGT Gly	TTC Phe	CGC Arg	TTT Phe 335	TTG Leu	1008
AGC Ser	GAC Asp	GAT Asp	AAA Lys 340	AAA Lys	GTT Val	GCG Ala	GTT Val	GTC Val 345	GGC Gly	AGC Ser	GCG Ala	AAA Lys	ACC Thr 350	AAA Lys	GAC Asp	1056
AAA Lys	ACG Thr	GAA Glu 355	AAT Asn	GGC Gly	GCG Ala	GTG Val	GCT Ala 360	TCA Ser	GGC Gly	GGC Gly	ACA Thr	GAT Asp 365	GCG Ala	GCA Ala	GCA Ala	1104
TCA Ser	AAC Asn 370	GGT Gly	GCG Ala	GCA Ala	GGC Gly	ACG Thr 375	TCG Ser	TCT Ser	GAA Glu	AAC Asn	AGT Ser 380	AAG Lys	CTG Leu	ACC Thr	ACG Thr	1152
GTT Val 385	TTG Leu	GAT Asp	GCG Ala	GTC Val	GAG Glu 390	CTG Leu	AAA Lys	TTG Leu	GGC Gly 395	GAT Asp	AAG Lys	GAA Glu	GTC Val	CAA Gln	AAG Lys 400	1200
CTC Leu	GAC Asp	AAC Asn	TTC Phe	AGC Ser 405	AAC Asn	GCC Ala	GCC Ala	CAA Gln	CTG Leu 410	GTT Val	GTC Val	GAC Asp	GGC Gly	ATT Ile 415	ATG Met	1248
ATT Ile	CCG Pro	CTC Leu	TTG Leu 420	CCC Pro	GAG Glu	GCT Ala	TCC Ser	GAA Glu 425	AGT Ser	GGG Gly	AAC Asn	AAT Asn	CAA Gln 430	GCC Ala	AAT Asn	1296
CAA Gln	GGT Gly	ACA Thr 435	AAT Asn	GGC Gly	GGA Gly	ACA Thr	GCC Ala 440	TTT Phe	ACC Thr	CGC Arg	AAA Lys	TTT Phe 445	GAC Asp	CAC His	ACG Thr	1344
CCG Pro	GAA Glu 450	AGT Ser	GAT Asp	AAA Lys	AAA Lys	GAC Asp 455	GCC Ala	CAA Gln	GCA Ala	GGT Gly	ACG Thr 460	CAG Gln	ACG Thr	AAT Asn	GGG Gly	1392
GCG Ala 465	CAA Gln	ACC Thr	GCT Ala	TCA Ser 470	AAT Asn	ACG Thr	GCA Ala	GGT Gly	GAT Asp	ACC Thr 475	AAT Asn	GGC Gly	AAA Lys	ACA Thr	AAA Lys 480	1440
ACC Thr	TAT Tyr	GAA Glu	GTC Val	GAA Glu 485	GTC Val	TGC Cys	TGT Cys	TCC Ser	AAC Asn 490	CTC Leu	AAT Asn	TAT Tyr	CTG Leu	AAA Lys 495	TAC Tyr	1488
GGA Gly	ATG Met	TTG Leu	ACG Thr 500	CGC Arg	AAA Lys	AAC Asn	AGC Ser	AAG Lys 505	TCC Ser	GCG Ala	ATG Met	CAG Gln	GCA Ala 510	GGA Gly	GAA Glu	1536
AGC Ser	AGT Ser	AGT Ser	CAA Gln 515	GCT Ala	GAT Asp	GCT Ala	AAA Lys 520	ACG Thr	GAA Glu	CAA Gln	GTT Val	GAA Glu 525	CAA Gln	AGT Ser	ATG Met	1584
TTC Phe	CTC Leu 530	CAA Gln	GGC Gly	GAG Glu	CGC Arg	ACC Thr 535	GAT Asp	GAA Glu	AAA Lys	GAG Glu	ATT Ile 540	CCA Pro	AGC Ser	GAG Glu	CAA Gln	1632
AAC Asn 545	ATC Ile	GTT Val	TAT Tyr	CGG Arg	GGG Gly 550	TCT Ser	TGG Trp	TAC Tyr	GGA Gly 555	TAT Tyr	ATT Ile	GCC Ala	AAC Asn	GAC Asp	AAA Lys 560	1680

AGC	ACA	AGC	TGG	AGC	GGC	AAT	GCT	TCC	AAT	GCA	ACG	AGT	GGC	AAC	AGG	1728
Ser	Thr	Ser	Trp	Ser	Gly	Asn	Ala	Ser	Asn	Ala	Thr	Ser	Gly	Asn	Arg	
				565					570					575		
GCG	GAA	TTT	ACT	GTG	AAT	TTT	GCC	GAT	AAA	AAA	ATT	ACT	GGT	ACG	TTA	1776
Ala	Glu	Phe	Thr	Val	Asn	Phe	Ala	Asp	Lys	Lys	Ile	Thr	Gly	Thr	Leu	
			580					585					590			
ACC	GCT	GAC	AAC	AGG	CAG	GAG	GCA	ACC	TTT	ACC	ATT	GAT	GGT	AAT	ATT	1824
Thr	Ala	Asp	Asn	Arg	Gln	Glu	Ala	Thr	Phe	Thr	Ile	Asp	Gly	Asn	Ile	
		595					600					605				
AAG	GAC	AAC	GGC	TTT	GAA	GGT	ACG	GCG	AAA	ACT	GCT	GAG	TCA	GGT	TTT	1872
Lys	Asp	Asn	Gly	Phe	Glu	Gly	Thr	Ala	Lys	Thr	Ala	Glu	Ser	Gly	Phe	
	610					615					620					
GAT	CTC	GAT	CAA	AGC	AAT	ACC	ACC	CGC	ACG	CCT	AAG	GCA	TAT	ATC	ACA	1920
Asp	Leu	Asp	Gln	Ser	Asn	Thr	Thr	Arg	Thr	Pro	Lys	Ala	Tyr	Ile	Thr	
					630					635					640	
GAT	GCC	AAG	GTG	CAG	GGC	GGT	TTT	TAC	GGG	CCC	AAA	GCC	GAA	GAG	TTG	1968
Asp	Ala	Lys	Val	Gln	Gly	Gly	Phe	Tyr	Gly	Pro	Lys	Ala	Glu	Glu	Leu	
				645					650					655		
GGC	GGA	TGG	TTT	GCC	TAT	CCG	GGC	GAT	AAA	CAA	ACG	AAA	AAT	GCA	ACA	2016
Gly	Gly	Trp	Phe	Ala	Tyr	Pro	Gly	Asp	Lys	Gln	Thr	Lys	Asn	Ala	Thr	
			660					665					670			
AAT	GCA	TCC	GGC	AAT	AGC	AGT	GCA	ACT	GTC	GTA	TTC	GGT	GCG	AAA	CGC	2064
Asn	Ala	Ser	Gly	Asn	Ser	Ser	Ala	Thr	Val	Val	Phe	Gly	Ala	Lys	Arg	
		675					680					685				
CAA	CAG	CCT	GTG	CGA	TAACGCAAGC	CCAAAAAGAC	CAAGGCGGAT	ACGGT								2114
Gln	Gln	Pro	Val	Arg												
			690													

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Cys	Leu	Gly	Gly	Gly	Gly	Thr	Phe	Asp	Leu	Asp	Ser	Val	Asp	Thr	Glu
1				5					10					15	
Ala	Pro	Arg	Pro	Asp	Pro	Lys	Tyr	Gln	Asp	Val	Ser	Ser	Glu	Lys	Pro
			20					25					30		
Gln	Ala	Gln	Lys	Asp	Gln	Gly	Gly	Tyr	Gly	Phe	Ala	Met	Arg	Leu	Lys
		35				40					45				
Arg	Arg	Asn	Trp	Tyr	Ser	Ala	Ala	Lys	Glu	Asp	Glu	Val	Lys	Leu	Asn
	50					55					60				

Glu 65	Ser	Asp	Trp	Glu	Thr 70	Thr	Gly	Leu	Pro	Thr 75	Glu	Pro	Lys	Lys	Leu 80
Pro	Leu	Lys	Gln	Glu 85	Ser	Val	Ile	Ser	Lys 90	Val	Gln	Ala	Asn	Asn	Gly 95
Asp	Asn	Asn	Ile 100	Tyr	Thr	Ser	Pro	Tyr 105	Leu	Thr	Gln	Ser	Asn	His	Gln
Asn	Ser	Ser 115	Ile	Asn	Gly	Gly	Ala 120	Asn	Leu	Pro	Lys	Asn	Glu	Val	Thr
Asn	Tyr 130	Lys	Asp	Phe	Lys	Tyr 135	Val	Tyr	Ser	Gly	Trp 140	Phe	Tyr	Lys	His
Ala 145	Lys	Asn	Glu	Ile	Ile 150	Arg	Glu	Asn	Ser	Ser 155	Ile	Lys	Gly	Ala	Lys 160
Asn	Gly	Asp	Asp	Gly 165	Tyr	Ile	Phe	Tyr	His 170	Gly	Lys	Glu	Pro	Ser	Arg 175
Gln	Leu	Pro	Ala 180	Ser	Gly	Thr	Val	Thr 185	Tyr	Lys	Gly	Val	Trp	His	Phe 190
Ala	Thr	Asp 195	Val	Lys	Lys	Ser	Gln 200	Asn	Phe	Arg	Asp	Ile 205	Ile	Gln	Pro
5 Ser	Lys	Lys	Gln	Gly	Asp	Arg 215	Tyr	Ser	Gly	Phe	Ser 220	Gly	Asp	Asp	Asp
Glu 225	Gln	Tyr	Ser	Asn	Lys 230	Asn	Glu	Ser	Met	Leu 235	Lys	Asp	Gly	Gln	Glu 240
Gly	Tyr	Gly	Phe	Thr 245	Ser	Asn	Leu	Glu	Val 250	Asp	Phe	Gly	Ser	Lys 255	Lys
Leu	Thr	Gly	Lys 260	Leu	Ile	Arg	Asn	Asn	Arg	Val	Thr	Asn	Ala	Pro	Thr
Asn	Asp	Lys 275	Tyr	Thr	Thr	Gln	Tyr 280	Tyr	Ser	Leu	Asp	Ala	Gln	Ile	Thr
Gly 290	Asn	Arg	Phe	Asn	Gly	Lys 295	Ala	Ile	Arg	Thr	Asp 300	Lys	Pro	Asp	Thr
Gly 305	Gly	Thr	Lys	Leu	His 310	Pro	Phe	Val	Ser	Asp 315	Ser	Ser	Ser	Leu	Ser 320
Gly	Gly	Phe	Phe	Gly 325	Pro	Lys	Gly	Glu	Glu 330	Leu	Gly	Phe	Arg	Phe	Leu 335
Ser	Asp	Asp	Lys 340	Lys	Val	Ala	Val	Val 345	Gly	Ser	Ala	Lys	Thr 350	Lys	Asp
Lys	Thr	Glu 355	Asn	Gly	Ala	Val	Ala 360	Ser	Gly	Gly	Thr	Asp 365	Ala	Ala	Ala
Ser	Asn	Gly	Ala	Ala	Gly	Thr 375	Ser	Ser	Glu	Asn	Ser 380	Lys	Leu	Thr	Thr

111

Val 385	Leu	Asp	Ala	Val	Glu 390	Leu	Lys	Leu	Gly	Asp 395	Lys	Glu	Val	Gln	Lys 400
Leu	Asp	Asn	Phe	Ser 405	Asn	Ala	Ala	Gln	Leu 410	Val	Val	Asp	Gly	Ile 415	Met
Ile	Pro	Leu	Leu 420	Pro	Glu	Ala	Ser	Glu 425	Ser	Gly	Asn	Asn	Gln	Ala	Asn
Gln	Gly	Thr 435	Asn	Gly	Gly	Thr	Ala 440	Phe	Thr	Arg	Lys	Phe 445	Asp	His	Thr
Pro	Glu 450	Ser	Asp	Lys	Lys	Asp 455	Ala	Gln	Ala	Gly	Thr 460	Gln	Thr	Asn	Gly
Ala 465	Gln	Thr	Ala	Ser	Asn 470	Thr	Ala	Gly	Asp	Thr 475	Asn	Gly	Lys	Thr	Lys
Thr	Tyr	Glu	Val	Glu 485	Val	Cys	Cys	Ser	Asn 490	Leu	Asn	Tyr	Leu	Lys	Tyr
Gly	Met	Leu	Thr 500	Arg	Lys	Asn	Ser	Lys 505	Ser	Ala	Met	Gln	Ala	Gly	Glu
Ser C5	Ser	Ser 515	Gln	Ala	Asp	Ala	Lys 520	Thr	Glu	Gln	Val	Glu 525	Gln	Ser	Met
Phe 530	Leu	Gln	Gly	Glu	Arg	Thr 535	Asp	Glu	Lys	Glu	Ile 540	Pro	Ser	Glu	Gln
Asn 545	Ile	Val	Tyr	Arg	Gly 550	Ser	Trp	Tyr	Gly	Tyr 555	Ile	Ala	Asn	Asp	Lys
Ser	Thr	Ser	Trp	Ser 565	Gly	Asn	Ala	Ser	Asn 570	Ala	Thr	Ser	Gly	Asn	Arg
Ala	Glu	Phe	Thr 580	Val	Asn	Phe	Ala	Asp 585	Lys	Lys	Ile	Thr	Gly	Thr	Leu
Thr	Ala	Asp 595	Asn	Arg	Gln	Glu	Ala 600	Thr	Phe	Thr	Ile	Asp 605	Gly	Asn	Ile
Lys 610	Asp	Asn	Gly	Phe	Glu	Gly 615	Thr	Ala	Lys	Thr	Ala 620	Glu	Ser	Gly	Phe
Asp 625	Leu	Asp	Gln	Ser	Asn 630	Thr	Thr	Arg	Thr	Pro 635	Lys	Ala	Tyr	Ile	Thr
Asp	Ala	Lys	Val	Gln 645	Gly	Gly	Phe	Tyr	Gly 650	Pro	Lys	Ala	Glu	Glu	Leu
Gly	Gly	Trp	Phe 660	Ala	Tyr	Pro	Gly	Asp 665	Lys	Gln	Thr	Lys	Asn	Ala	Thr
Asn	Ala	Ser 675	Gly	Asn	Ser	Ser	Ala 680	Thr	Val	Val	Phe	Gly 685	Ala	Lys	Arg
Gln 690	Gln	Pro	Val	Arg											

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: S3032

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..2097

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2097

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGT	TTG	GGC	GGA	GGC	GGC	GGC	AGT	TTC	GAT	CTT	GAT	TCT	GTC	GAT	ACC	48
Cys	Leu	Gly	Gly	Gly	Gly	Gly	Ser	Phe	Asp	Leu	Asp	Ser	Val	Asp	Thr	
1				5					10					15		
GAA	GCC	CCG	CGT	CCC	GCG	CCA	AAG	TAT	CAA	GAT	GTT	TCT	TCC	GAA	AAA	96
Glu	Ala	Pro	Arg	Pro	Ala	Pro	Lys	Tyr	Gln	Asp	Val	Ser	Ser	Glu	Lys	
			20					25					30			
CCG	CAA	GCC	CAA	AAA	GAC	CAA	GGC	GGA	TAC	GGT	TTT	GCG	ATG	AGG	TTG	144
Pro	Gln	Ala	Gln	Lys	Asp	Gln	Gly	Gly	Tyr	Gly	Phe	Ala	Met	Arg	Leu	
			35				40					45				
AAA	CGG	AGG	AAT	TGG	TAT	CCG	TCG	GCA	AAA	GAA	AAC	GAG	GTT	AAA	CTG	192
Lys	Arg	Arg	Asn	Trp	Tyr	Pro	Ser	Ala	Lys	Glu	Asn	Glu	Val	Lys	Leu	
	50					55					60					
AAT	GAG	AGT	GAT	TGG	GAG	ACG	ACA	GGA	TTG	CCA	AGC	AAT	CCC	AAA	AAC	240
Asn	Glu	Ser	Asp	Trp	Glu	Thr	Thr	Gly	Leu	Pro	Ser	Asn	Pro	Lys	Asn	
	65			70					75					80		
TTA	CCT	GAG	CGA	CAG	AAA	TCG	GTT	ATT	GAT	CAA	GTA	GAA	ACA	GAT	GGC	288
Leu	Pro	Glu	Arg	Gln	Lys	Ser	Val	Ile	Asp	Gln	Val	Glu	Thr	Asp	Gly	
				85					90					95		
GAC	AGC	AAT	AAC	AGC	AAT	ATT	TAT	TCT	TCC	CCC	TAT	CTC	ACG	CAA	TCA	336
Asp	Ser	Asn	Asn	Ser	Asn	Ile	Tyr	Ser	Ser	Pro	Tyr	Leu	Thr	Gln	Ser	
			100					105					110			
AAC	CAT	CAA	AAC	GGC	AAC	ACT	GGC	AAC	GGT	GTA	AAC	CAA	CCA	AAA	AAC	384
Asn	His	Gln	Asn	Gly	Asn	Thr	Gly	Asn	Gly	Val	Asn	Gln	Pro	Lys	Asn	
			115				120					125				
GAA	GTA	ACA	GAT	TAC	AAA	AAT	TTT	AAA	TAT	GTT	TAT	TCC	GGC	TGG	TTT	432
Glu	Val	Thr	Asp	Tyr	Lys	Asn	Phe	Lys	Tyr	Val	Tyr	Ser	Gly	Trp	Phe	

130	135	140	
TAC AAA CAC GCC AAA CGA GAG GTT AAC TTA GCG GTG GAA CCT AAA ATT Tyr Lys His Ala Lys Arg Glu Val Asn Leu Ala Val Glu Pro Lys Ile 145 150 155 160	480		
GCA AAA AAC GGC GAC GAC GGT TAT ATC TTC TAT CAC GGT AAA GAC CCT Ala Lys Asn Gly Asp Asp Gly Tyr Ile Phe Tyr His Gly Lys Asp Pro 165 170 175	528		
TCC CGA CAA CTT CCC GCT TCT GGA AAA ATT ACC TAT AAA GGT GTG TGG Ser Arg Gln Leu Pro Ala Ser Gly Lys Ile Thr Tyr Lys Gly Val Trp 180 185 190	576		
CAT TTT GCG ACC GAT ACA AAA AGG GGT CAA AAA TTT CGT GAA ATT ATC His Phe Ala Thr Asp Thr Lys Arg Gly Gln Lys Phe Arg Glu Ile Ile 195 200 205	624		
CAA CCT TCA AAA AAT CAA GGC GAC AGA TAT AGC GGA TTT TCG GGT GAT Gln Pro Ser Lys Asn Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp 210 215 220	672		
GAT GAT GAA CAA TAT TCT AAT AAA AAC GAA TCC ATG CTG AAA GAT GGT Asp Asp Glu Gln Tyr Ser Asn Lys Asn Glu Ser Met Leu Lys Asp Gly 225 230 235 240	720		
CAT GAA GGT TAT GGT TTT GCC TCG AAT TTA GAA GTG GAT TTC GAC AAT His Glu Gly Tyr Gly Phe Ala Ser Asn Leu Glu Val Asp Phe Asp Asn 245 250 255	768		
AAA AAA TTG ACG GGT AAA TTA ATA CGC AAT AAT GCG AAC CAA AAT AAT Lys Lys Leu Thr Gly Lys Leu Ile Arg Asn Asn Ala Asn Gln Asn Asn 260 265 270	816		
AAT ACT AAT AAT GAC AAA CAC ACC ACC CAA TAC TAC AGC CTT GAT GCG Asn Thr Asn Asn Asp Lys His Thr Thr Gln Tyr Tyr Ser Leu Asp Ala 275 280 285	864		
ACG CTT AAG GGA AAC CGC TTC AGC GGA AAA GCG GAA GCA ACC GAC AAA Thr Leu Lys Gly Asn Arg Phe Ser Gly Lys Ala Glu Ala Thr Asp Lys 290 295 300	912		
CCC AAA AAC GAC GGC GAA ACC AAG GAA CAT CCC TTT GTT TCC GAC TCG Pro Lys Asn Asp Gly Glu Thr Lys Glu His Pro Phe Val Ser Asp Ser 305 310 315 320	960		
TCT TCT TTG AGC GGC GGC TTT TTC GGC CCG CAG GGT GAG GAA TTG GGT Ser Ser Leu Ser Gly Gly Phe Phe Gly Pro Gln Gly Glu Glu Leu Gly 325 330 335	1008		
TTC CGC TTT TTG AGC AAC GAT CAA AAA GTT GCC GTT GTC GGC AGC GCG Phe Arg Phe Leu Ser Asn Asp Gln Lys Val Ala Val Val Gly Ser Ala 340 345 350	1056		
AAA ACC AAA GAC AAA CCC GCA AAT GGC AAT ACT GCG GAG GCT TCA GGC Lys Thr Lys Asp Lys Pro Ala Asn Gly Asn Thr Ala Glu Ala Ser Gly 355 360 365	1104		
GGC ACA GAT GCG GCA GCA TCG GGC GGT GCG GCA GGC ACG TCG TCT GAA Gly Thr Asp Ala Ala Ala Ser Gly Gly Ala Ala Gly Thr Ser Ser Glu 1152			

370

375

380

AAC Asn 385	AGT Ser	AAG Lys	CTG Leu	ACC Thr	ACG Thr 390	GTT Val	TTG Leu	GAT Asp	GCG Ala	GTC Val 395	GAG Glu	CTG Leu	ACG Thr	CAC His	GGC Gly 400	1200
GGC Gly	ACA Thr	GCA Ala	ATC Ile	AAA Lys 405	AAT Asn	CTC Leu	GAC Asp	AAC Asn	TTC Phe 410	AGC Ser	AAT Asn	GCC Ala	GCC Ala	CAA Gln 415	CTG Leu	1248
GTT Val	GTC Val	GAC Asp	GGC Gly 420	ATT Ile	ATG Met	ATT Ile	CCG Pro	CTC Leu 425	CTG Leu	CCT Pro	CAA Gln	AAT Asn	TCA Ser 430	ACA Thr	GGC Gly	1296
AAA Lys	AAT Asn	AAT Asn 435	CAG Gln	CCC Pro	GAT Asp	CAA Gln	GGT Gly 440	AAA Lys	AAC Asn	GGC Gly	GGA Gly	ACA Thr 445	GCC Ala	TTT Phe	ATC Ile	1344
TAT Tyr	AAA Lys 450	ACG Thr	ACC Thr	TAC Tyr	ACG Thr	CCG Pro 455	AAA Lys	AAC Asn	GAT Asp	GAC Asp	AAA Lys 460	GAT Asp	ACC Thr	AAA Lys	GCC Ala	1392
CAA Gln 465	ACA Thr	GTC Val	ACG Thr	GGC Gly	GGC Gly 470	ACG Thr	CAA Gln	ACC Thr	GCT Ala	TCA Ser 475	AAT Asn	ACG Thr	GCA Ala	GGT Gly	GAT Asp 480	1440
GCC Ala	AAT Asn	GGC Gly	AAA Lys	ACA Thr 485	AAA Lys	ACC Thr	TAT Tyr	GAA Glu	GTC Val 490	GAA Glu	GTC Val	TGC Cys	TGT Cys	TCC Ser 495	AAC Asn	1488
CTC Leu	AAT Asn	TAT Tyr	CTG Leu 500	AAA Lys	TAC Tyr	GGG Gly	TTG Leu	CTG Leu 505	ACG Thr	CGC Arg	AAA Lys	ACT Thr	GCC Ala 510	GGC Gly	AAC Asn	1536
ACG Thr	GTG Val	GGA Gly 515	AGC Ser	GGC Gly	AAC Asn	AGC Ser	AGC Ser 520	CCA Pro	ACC Thr	GCC Ala	GCC Ala	GCC Ala 525	CAA Gln	ACG Thr	GAC Asp	1584
GCG Ala 530	CAG Gln	AGT Ser	ATG Met	TTC Phe	CTC Leu	CAA Gln 535	GGC Gly	GAG Glu	CGC Arg	ACC Thr	GAT Asp 540	GAA Glu	AAC Asn	AAG Lys	ATT Ile	1632
CCA Pro 545	AGC Ser	GAG Glu	CAA Gln	AAC Asn	GTC Val 550	GTT Val	TAT Tyr	CGG Arg	GGG Gly	TCT Ser 555	TGG Trp	TAC Tyr	GGG Gly	CAT His	ATT Ile 560	1680
GCC Ala	AGC Ser	AGC Ser	ACA Thr	AGC Ser 565	TGG Trp	AGC Ser	GGC Gly	AAT Asn	GCT Ala 570	TCT Ser	GAT Asp	AAA Lys	GAG Glu	GGC Gly 575	GGC Gly	1728
AAC Asn	AGG Arg	GCG Ala	GAA Glu 580	TTT Phe	ACT Thr	GTG Val	AAT Asn	TTT Phe 585	GGC Gly	GAG Glu	AAA Lys	AAA Lys	ATT Ile 590	ACC Thr	GGC Gly	1776
ACG Thr	TTA Leu	ACC Thr 595	GCT Ala	GAA Glu	AAC Asn	AGG Arg	CAG Gln 600	GAG Glu	GCA Ala	ACC Thr	TTT Phe 605	ACC Thr	ATT Ile	GAT Asp	GGT Gly	1824
AAG Lys	ATT Ile	GAG Glu	GGC Gly	AAC Asn	GGT Gly	TTT Phe	TCC Ser	GGT Gly	ACG Thr	GCA Ala	AAA Lys	ACT Thr	GCT Ala	GAA Glu	TTA Leu	1872

610	615	620	
GGT TTT GAT CTC GAT CAA AAA AAT ACC ACC CGC AC	GGT TTT GAT CTC GAT CAA AAA AAT ACC ACC CGC AC	GGT TTT GAT CTC GAT CAA AAA AAT ACC ACC CGC AC	1920
Gly Phe Asp Leu Asp Gln Lys Asn Thr Thr Arg Thr	Gly Phe Asp Leu Asp Gln Lys Asn Thr Thr Arg Thr	Gly Phe Asp Leu Asp Gln Lys Asn Thr Thr Arg Thr	
625	630	635	640
ATC ACA GAT GCC AAG GTA AAG GGC GGT TTT TAC GGG CCC AAA GCC GAA	ATC ACA GAT GCC AAG GTA AAG GGC GGT TTT TAC GGG CCC AAA GCC GAA	ATC ACA GAT GCC AAG GTA AAG GGC GGT TTT TAC GGG CCC AAA GCC GAA	1968
Ile Thr Asp Ala Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys Ala Glu	Ile Thr Asp Ala Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys Ala Glu	Ile Thr Asp Ala Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys Ala Glu	
	645	650	655
GAG TTG GGC GGA TGG TTT GCC TAT TCG GAC GAT AAA CAA ACG AAA AAT	GAG TTG GGC GGA TGG TTT GCC TAT TCG GAC GAT AAA CAA ACG AAA AAT	GAG TTG GGC GGA TGG TTT GCC TAT TCG GAC GAT AAA CAA ACG AAA AAT	2016
Glu Leu Gly Gly Trp Phe Ala Tyr Ser Asp Asp Lys Gln Thr Lys Asn	Glu Leu Gly Gly Trp Phe Ala Tyr Ser Asp Asp Lys Gln Thr Lys Asn	Glu Leu Gly Gly Trp Phe Ala Tyr Ser Asp Asp Lys Gln Thr Lys Asn	
	660	665	670
GCA ACA GAT GCA TCC GGC AAT GGA AAT TCA GCA AGC AGT GCA ACT GTC	GCA ACA GAT GCA TCC GGC AAT GGA AAT TCA GCA AGC AGT GCA ACT GTC	GCA ACA GAT GCA TCC GGC AAT GGA AAT TCA GCA AGC AGT GCA ACT GTC	2064
Ala Thr Asp Ala Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala Thr Val	Ala Thr Asp Ala Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala Thr Val	Ala Thr Asp Ala Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala Thr Val	
	675	680	685
GTA TTC GGT GCG AAA CGC CAA CAG CCT GTG CAA TAAACCAAGG CGGATAC	GTA TTC GGT GCG AAA CGC CAA CAG CCT GTG CAA TAAACCAAGG CGGATAC	GTA TTC GGT GCG AAA CGC CAA CAG CCT GTG CAA TAAACCAAGG CGGATAC	2114
Val Phe Gly Ala Lys Arg Gln Gln Pro Val Gln	Val Phe Gly Ala Lys Arg Gln Gln Pro Val Gln	Val Phe Gly Ala Lys Arg Gln Gln Pro Val Gln	
690	695		

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Cys	Leu	Gly	Gly	Gly	Gly	Gly	Ser	Phe	Asp	Leu	Asp	Ser	Val	Asp	Thr
1				5					10					15	
Glu	Ala	Pro	Arg	Pro	Ala	Pro	Lys	Tyr	Gln	Asp	Val	Ser	Ser	Glu	Lys
			20					25					30		
Pro	Gln	Ala	Gln	Lys	Asp	Gln	Gly	Gly	Tyr	Gly	Phe	Ala	Met	Arg	Leu
			35				40					45			
Lys	Arg	Arg	Asn	Trp	Tyr	Pro	Ser	Ala	Lys	Glu	Asn	Glu	Val	Lys	Leu
	50					55					60				
Asn	Glu	Ser	Asp	Trp	Glu	Thr	Thr	Gly	Leu	Pro	Ser	Asn	Pro	Lys	Asn
	65				70					75				80	
Leu	Pro	Glu	Arg	Gln	Lys	Ser	Val	Ile	Asp	Gln	Val	Glu	Thr	Asp	Gly
				85					90					95	
Asp	Ser	Asn	Asn	Ser	Asn	Ile	Tyr	Ser	Ser	Pro	Tyr	Leu	Thr	Gln	Ser
			100					105					110		
Asn	His	Gln	Asn	Gly	Asn	Thr	Gly	Asn	Gly	Val	Asn	Gln	Pro	Lys	Asn
			115				120					125			
Glu	Val	Thr	Asp	Tyr	Lys	Asn	Phe	Lys	Tyr	Val	Tyr	Ser	Gly	Trp	Phe
	130					135						140			

116

Tyr	Lys	His	Ala	Lys	Arg	Glu	Val	Asn	Leu	Ala	Val	Glu	Pro	Lys	Ile	145	150	155	160
Ala	Lys	Asn	Gly	Asp	Asp	Gly	Tyr	Ile	Phe	Tyr	His	Gly	Lys	Asp	Pro	165	170	175	
Ser	Arg	Gln	Leu	Pro	Ala	Ser	Gly	Lys	Ile	Thr	Tyr	Lys	Gly	Val	Trp	180	185	190	
His	Phe	Ala	Thr	Asp	Thr	Lys	Arg	Gly	Gln	Lys	Phe	Arg	Glu	Ile	Ile	195	200	205	
Gln	Pro	Ser	Lys	Asn	Gln	Gly	Asp	Arg	Tyr	Ser	Gly	Phe	Ser	Gly	Asp	210	215	220	
Asp	Asp	Glu	Gln	Tyr	Ser	Asn	Lys	Asn	Glu	Ser	Met	Leu	Lys	Asp	Gly	225	230	235	240
His	Glu	Gly	Tyr	Gly	Phe	Ala	Ser	Asn	Leu	Glu	Val	Asp	Phe	Asp	Asn	245	250	255	
Lys	Lys	Leu	Thr	Gly	Lys	Leu	Ile	Arg	Asn	Asn	Ala	Asn	Gln	Asn	Asn	260	265	270	
Asn	Thr	Asn	Asn	Asp	Lys	His	Thr	Thr	Gln	Tyr	Tyr	Ser	Leu	Asp	Ala	275	280	285	
CS Thr	Leu	Lys	Gly	Asn	Arg	Phe	Ser	Gly	Lys	Ala	Glu	Ala	Thr	Asp	Lys	290	295	300	
Pro	Lys	Asn	Asp	Gly	Glu	Thr	Lys	Glu	His	Pro	Phe	Val	Ser	Asp	Ser	305	310	315	320
Ser	Ser	Leu	Ser	Gly	Gly	Phe	Phe	Gly	Pro	Gln	Gly	Glu	Glu	Leu	Gly	325	330	335	
Phe	Arg	Phe	Leu	Ser	Asn	Asp	Gln	Lys	Val	Ala	Val	Val	Gly	Ser	Ala	340	345	350	
Lys	Thr	Lys	Asp	Lys	Pro	Ala	Asn	Gly	Asn	Thr	Ala	Glu	Ala	Ser	Gly	355	360	365	
Gly	Thr	Asp	Ala	Ala	Ala	Ser	Gly	Gly	Ala	Ala	Gly	Thr	Ser	Ser	Glu	370	375	380	
Asn	Ser	Lys	Leu	Thr	Thr	Val	Leu	Asp	Ala	Val	Glu	Leu	Thr	His	Gly	385	390	395	400
Gly	Thr	Ala	Ile	Lys	Asn	Leu	Asp	Asn	Phe	Ser	Asn	Ala	Ala	Gln	Leu	405	410	415	
Val	Val	Asp	Gly	Ile	Met	Ile	Pro	Leu	Leu	Pro	Gln	Asn	Ser	Thr	Gly	420	425	430	
Lys	Asn	Asn	Gln	Pro	Asp	Gln	Gly	Lys	Asn	Gly	Gly	Thr	Ala	Phe	Ile	435	440	445	
Tyr	Lys	Thr	Thr	Tyr	Thr	Pro	Lys	Asn	Asp	Asp	Lys	Asp	Thr	Lys	Ala	450	455	460	

Gln Thr Val Thr Gly Gly Thr Gln Thr Ala Ser Asn Thr Ala Gly Asp
 465 470 475 480
 Ala Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn
 485 490 495
 Leu Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn
 500 505 510
 Thr Val Gly Ser Gly Asn Ser Ser Pro Thr Ala Ala Ala Gln Thr Asp
 515 520 525
 Ala Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Asn Lys Ile
 530 535 540
 Pro Ser Glu Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile
 545 550 555 560
 Ala Ser Ser Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly
 565 570 575
 Asn Arg Ala Glu Phe Thr Val Asn Phe Gly Glu Lys Lys Ile Thr Gly
 580 585 590
 C5 Thr Leu Thr Ala Glu Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp Gly
 595 600 605
 Lys Ile Glu Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Glu Leu
 610 615 620
 Gly Phe Asp Leu Asp Gln Lys Asn Thr Thr Arg Thr Pro Lys Ala Tyr
 625 630 635 640
 Ile Thr Asp Ala Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys Ala Glu
 645 650 655
 Glu Leu Gly Gly Trp Phe Ala Tyr Ser Asp Asp Lys Gln Thr Lys Asn
 660 665 670
 Ala Thr Asp Ala Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala Thr Val
 675 680 685
 Val Phe Gly Ala Lys Arg Gln Gln Pro Val Gln
 690 695

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: IM2169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Thr Lys Asp Lys Leu Glu Asn Gly Ala Ala Ala Ser Gly Ser Thr Gly
1 5 10 15
Ala Ala Ala Ser Gly Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys
20 25 30
Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys
35 40 45
Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
50 55 60
Gly Ile Met Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly Asn Thr
65 70 75 80
Gln Ala Asp Lys Gly Lys Asn Gly Gly Thr Glu Phe Thr Arg Lys Phe
85 90 95
Glu His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln
100 105 110
Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
115 120 125
Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
130 135 140
Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln
145 150 155 160
Ala Gly Gly Asn Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu
165 170 175
Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro
180 185 190
Thr Asp Gln Asn Val Val
195

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: 6940

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Thr Lys Asp Lys Thr Glu Asn Gly Ala Val Ala Ser Gly Gly Thr Asp

1		5		10		15									
Ala	Ala	Ala	Ser	Asn	Gly	Ala	Ala	Gly	Thr	Ser	Ser	Glu	Asn	Ser	Lys
		20						25					30		
Leu	Thr	Thr	Val	Leu	Asp	Ala	Val	Glu	Leu	Lys	Leu	Gly	Asp	Lys	Glu
		35					40					45			
Val	Gln	Lys	Leu	Asp	Asn	Phe	Ser	Asn	Ala	Ala	Gln	Leu	Val	Val	Asp
	50					55					60				
Gly	Ile	Met	Ile	Pro	Leu	Leu	Pro	Glu	Ala	Ser	Glu	Ser	Gly	Asn	Asn
65					70					75					80
Gln	Ala	Asn	Gln	Gly	Thr	Asn	Gly	Gly	Thr	Ala	Phe	Thr	Arg	Lys	Phe
			85						90					95	
Asp	His	Thr	Pro	Glu	Ser	Asp	Lys	Lys	Asp	Ala	Gln	Ala	Gly	Thr	Gln
			100					105					110		
Thr	Asn	Gly	Ala	Gln	Thr	Ala	Ser	Asn	Thr	Ala	Gly	Asp	Thr	Asn	Gly
		115					120					125			
Lys	Thr	Lys	Thr	Tyr	Glu	Val	Glu	Val	Cys	Cys	Ser	Asn	Leu	Asn	Tyr
	130					135					140				
Leu	Lys	Tyr	Gly	Met	Leu	Thr	Arg	Lys	Asn	Ser	Lys	Ser	Ala	Met	Gln
145					150					155					160
Ala	Gly	Glu	Ser	Ser	Ser	Gln	Ala	Asp	Ala	Lys	Thr	Glu	Gln	Val	Glu
			165					170						175	
Gln	Ser	Met	Phe	Leu	Gln	Gly	Glu	Arg	Thr	Asp	Glu	Lys	Glu	Ile	Pro
			180					185					190		
Ser	Glu	Gln	Asn	Ile	Val										
			195												

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: 2223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Thr	Lys	Asp	Lys	Thr	Glu	Asn	Gly	Ala	Val	Ala	Ser	Gly	Gly	Thr	Asp
1				5					10					15	
Ala	Ala	Ala	Ser	Asn	Gly	Ala	Ala	Gly	Thr	Ser	Ser	Glu	Asn	Ser	Lys
			20					25					30		

120

Leu Thr Thr Val Leu Asp Ala Val Glu Leu Lys Leu Gly Asp Lys Glu
 35 40 45
 Val Gln Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
 50 55 60
 Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Asn Asn
 65 70 75 80
 Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
 85 90 95
 Asp His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln
 100 105 110
 Ala Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
 115 120 125
 Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
 130 135 140
 Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln
 145 150 155 160
 Ala Gly Glu Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Gly
 165 170 175
 Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro
 180 185 190
 Ser Glu Gln Asn Ile Val
 195

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *N. meningitidis*
- (B) STRAIN: C708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Thr Gln Asp Lys Pro Arg Asn Gly Ala Val Ala Ser Gly Gly Thr Gly
 1 5 10 15
 Ala Ala Arg Ser Asn Gly Ala Ala Gly Gln Ser Ser Glu Asn Ser Lys
 20 25 30
 Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys
 35 40 45

Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
 50 55 60
 Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Lys Asn
 65 70 75 80
 Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
 85 90 95
 Asn His Thr Pro Lys Ser Asp Glu Lys Asp Thr Gln Ala Gly Thr Ala
 100 105 110
 Glu Asn Gly Asn Pro Ala Ala Ser Asn Thr Ala Gly Asp Ala Asn Gly
 115 120 125
 Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
 130 135 140
 Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln
 145 150 155 160
 Ala Gly Glu Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Gly
 165 170 175
 Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro
 180 185 190
 Asn Asp Gln Asn Val Val
 195

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *N. meningitidis*
- (B) STRAIN: M978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Thr Gln Asp Lys Ala Ala Asn Gly Asn Thr Ala Ala Ala Ser Gly Gly
 1 5 10 15
 Thr Asp Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn
 20 25 30
 Ser Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp
 35 40 45
 Lys Lys Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
 50 55 60
 Val Asp Gly Ile Met Ile Pro Leu Leu Pro Glu Thr Ser Glu Ser Gly

65		70		75		80									
Ser	Asn	Gln	Ala	Asp	Lys	Gly	Lys	Lys	Gly	Lys	Asn	Gly	Lys	Asn	Gly
				85					90					95	
Gly	Thr	Asp	Phe	Thr	Tyr	Lys	Thr	Thr	Tyr	Thr	Pro	Lys	Asn	Asp	Asp
			100					105					110		
Lys	Asp	Thr	Lys	Ala	Gln	Thr	Gly	Ala	Ala	Gly	Ser	Ser	Gly	Ala	Gln
		115					120					125			
Thr	Asp	Leu	Gly	Lys	Ala	Asp	Val	Asn	Gly	Gly	Lys	Ala	Glu	Thr	Lys
	130					135					140				
Thr	Tyr	Glu	Val	Glu	Val	Cys	Cys	Ser	Asn	Leu	Asn	Tyr	Leu	Lys	Tyr
145					150					155					160
Gly	Met	Leu	Thr	Arg	Lys	Asn	Ser	Lys	Ser	Ala	Met	Gln	Ala	Gly	Gly
				165					170					175	
Asn	Ser	Ser	Gln	Ala	Asp	Ala	Lys	Thr	Glu	Gln	Val	Glu	Gln	Ser	Met
			180					185					190		
Phe	Leu	Gln	Gly	Glu	Arg	Thr	Asp	Glu	Lys	Glu	Ile	Pro	Asn	Asp	Gln
		195					200					205			
Asn	Val	Val													
		210													

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: 1610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Lys	Arg	Asp	Lys	Ala	Glu	Ser	Gly	Gly	Gly	Asn	Gly	Ala	Ser	Gly	Gly
1				5					10					15	
Thr	Asp	Ala	Ala	Ala	Ser	Asn	Gly	Ala	Ala	Gly	Thr	Ser	Ser	Glu	Asn
		20						25					30		
Ser	Lys	Leu	Thr	Thr	Val	Leu	Asp	Ala	Val	Glu	Leu	Lys	Ser	Gly	Gly
		35					40					45			
Lys	Glu	Val	Lys	Asn	Leu	Asp	Asn	Phe	Ser	Asn	Ala	Ala	Gln	Leu	Val
	50					55					60				
Val	Asp	Gly	Ile	Met	Ile	Pro	Leu	Leu	Pro	Lys	Asp	Ser	Glu	Ser	Gly
65					70					75					80

Asn Thr Gln Ala Asp Lys Gly Lys Asn Gly Gly Thr Lys Phe Thr Arg
 85 90 95
 Lys Phe Glu His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly
 100 105 110
 Thr Gln Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr
 115 120 125
 Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu
 130 135 140
 Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn Thr
 145 150 155 160
 Gly Glu Gly Gly Asn Gly Ser Gln Thr Ala Ala Ala Gln Thr Ala Gln
 165 170 175
 Gly Ala Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu
 180 185 190
 Ile Pro Ser Glu Gln Asn Val Val
 195 200

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: 867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Thr Lys Asp Lys Pro Arg Asn Gly Ala Val Ala Ser Gly Gly Thr Asp
 1 5 10 15
 Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Gly Lys
 20 25 30
 Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys
 35 40 45
 Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Ala
 50 55 60
 Gly Ile Met Ile Pro Leu Met Pro Glu Thr Ser Glu Ser Gly Asn Asn
 65 70 75 80
 Gln Ala Asp Leu Gly Leu Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
 85 90 95

Asp His Thr Pro Lys Ser Asp Glu Lys Asp Thr Gln Ala Gly Thr Pro
 100 105 110
 Thr Asn Gly Ala Gln Thr Ala Ser Gly Thr Ala Gly Val Thr Gly Gly
 115 120 125
 Gln Ala Gly Lys Thr Tyr Ala Val Glu Val Cys Cys Ser Asn Leu Asn
 130 135 140
 Tyr Leu Lys Thr Gly Leu Leu Thr Arg Lys Thr Ala Asp Asn Thr Val
 145 150 155 160
 Gly Ser Gly Asn Gly Ser Ser Thr Ala Ala Ala Gln Thr Ala Gln Gly
 165 170 175
 Ala Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile
 180 185 190
 Pro Lys Glu Gln Gln Asp Ile Val
 195

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
 (B) STRAIN: S3032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Thr Lys Asp Lys Pro Ala Asn Gly Asn Thr Ala Glu Ala Ser Gly Gly
 1 5 10 15
 Thr Asp Ala Ala Ala Ser Gly Gly Ala Ala Gly Thr Ser Ser Glu Asn
 20 25 30
 Ser Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr His Gly Gly
 35 40 45
 Thr Ala Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
 50 55 60
 Val Asp Gly Ile Met Ile Pro Leu Leu Pro Gln Asn Ser Thr Gly Lys
 65 70 75 80
 Asn Asn Gln Pro Asp Gln Gly Lys Asn Gly Gly Thr Ala Phe Ile Thr
 85 90 95
 Leu Thr Thr Tyr Thr Pro Lys Asn Asp Asp Lys Asp Thr Lys Ala Gln
 100 105 110
 Thr Val Thr Gly Gly Thr Gln Thr Ala Ser Asn Thr Ala Gly Asp Ala

115

120

125

Asn	Gly	Lys	Thr	Lys	Thr	Tyr	Glu	Val	Glu	Val	Cys	Cys	Ser	Asn	Leu
130						135					140				
Asn	Tyr	Leu	Lys	Thr	Gly	Leu	Leu	Thr	Arg	Lys	Thr	Ala	Gly	Asn	Thr
145					150					155					160
Val	Gly	Ser	Gly	Asn	Ser	Ser	Pro	Thr	Ala	Ala	Ala	Gln	Thr	Asp	Ala
				165					170					175	
Gln	Ser	Met	Phe	Leu	Gln	Gly	Glu	Arg	Thr	Asp	Glu	Asn	Lys	Ile	Pro
			180					185					190		
Ser	Glu	Gln	Asn	Val	Val										

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
 (B) STRAIN: 891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Thr	Lys	Asp	Lys	Pro	Gly	Asn	Gly	Ala	Arg	Leu	Gln	Ala	Ala	Arg	Cys
1				5					10					15	
Gly	Thr	Ser	Asn	Gly	Ala	Ala	Gly	Gln	Ser	Ser	Glu	Asn	Ser	Lys	Leu
			20					25					30		
Thr	Thr	Val	Leu	Asp	Ala	Val	Glu	Leu	Lys	Leu	Gly	Asp	Lys	Glu	Val
		35					40					45			
Gln	Lys	Leu	Asp	Asn	Phe	Ser	Asn	Ala	Ala	Gln	Leu	Val	Val	Asp	Gly
	50					55					60				
Ile	Met	Ile	Pro	Leu	Leu	Pro	Lys	Asp	Ser	Glu	Ser	Gly	Lys	Asn	Gln
65					70					75					80
Ala	Asp	Lys	Gly	Lys	Asn	Gly	Glu	Thr	Glu	Phe	Thr	Arg	Lys	Phe	Glu
				85					90					95	
His	Thr	Pro	Glu	Ser	Asp	Glu	Lys	Asp	Ala	Gln	Ala	Gly	Thr	Pro	Ser
			100					105					110		
Asn	Gly	Ala	Gln	Thr	Ala	Ser	Asn	Thr	Ala	Gly	Asp	Thr	Asn	Gly	Lys
		115					120					125			
Thr	Lys	Thr	Tyr	Glu	Val	Asn	Leu	Cys	Ser	Asn	Leu	Asn	Tyr	Leu	Lys

126

130

135

140

Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn Thr Gly Glu Gly Gly
145 150 155 160

Asn Ser Ser Pro Thr Ala Ala Gln Thr Ala Gln Gly Ala Gln Ser Met
165 170 175

Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Asn Asp Gln
180 185 190

Asn Val Val
195

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AAACCCGGAT CCGTTGCCAG CGCTGCCGT

29

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TTTTTTCATG AGATATCTGG CAACATTGTT GTTATCTCTG GCGGTGTTAA TCACCGCCGG

60

GTGCCTGGGT GCGGCGGCA GTTTC

85

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GTGTTTTTGT TGAGTGCATG CCTGGGTGGC

30

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TGCGCAAGCT TACAGTTTGT CTTTGGTTTT CGCGCTGCCG

40

(2) INFORMATION FOR SEQ ID NO:24:

/ (i) SEQUENCE CHARACTERISTICS:

- 
- (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AAAAAGCATG CATAAAACT ACGCGTTACA CCATTCAAGC

40

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TATATAAGCT TACGTTGCAG GCCCTGCCGC GTTTTCCCC

39

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CCCGAATTCT GCCGTCTGAA GCCTTATTC

29

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCCGAATTCT GCTATGGTGC TGCCTGTG

28

(2) INFORMATION FOR SEQ ID NO:28:

✓ (i) SEQUENCE CHARACTERISTICS:

- 5
- (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CGCATCCAAA ACCGTACCTG TGCTGCCTGA

30

(2) INFORMATION FOR SEQ ID NO:29

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TTTATCACTT TCCGGGGGCA GGAGCGGAAT

30

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs

129

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GTTGGAACAG CAGACAGCGG TTTGCGCCCC

30

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GAACATACTT TGTTCGTTTT TGCGCGTCAA

30

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: IM2394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Tyr Lys Gly Thr Trp
1 5

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis

(B) STRAIN: IM2394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Glu Phe Glu Val Asp Phe Ser Asp Lys Thr Ile Lys Gly Thr Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: IM2394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Glu Gly Gly Phe Tyr Gly Pro Lys Gly Glu Glu Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: IM2394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Ala Val Phe Gly Ala Lys
1 5

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..2067

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 1..60

5 (ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 61..2067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

ATG AAC AAT CCA TTG GTA AAT CAG GCT GCT ATG GTG CTG CCT GTG TTT	48
Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe	
-20 -15 -10 -5	
TTG TTG AGT GCT TGT CTG GGC GGA GGC GGC AGT TTC GAT CTT GAT TCT	96
Leu Leu Ser Ala Cys Leu Gly Gly Gly Ser Phe Asp Leu Asp Ser	
1 5 10	
GTC GAT ACC GAA GCC CCG CGT CCC GCG CCA AAG TAT CAA GAT GTT TCT	144
Val Asp Thr Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser	
15 20 25	
TCC GAA ACA CCG CAA GCC CAA AAA GAC CAA GGC GGA TAC GGT TTT GCA	192
Ser Glu Thr Pro Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala	
30 35 40	
ATG CGC TTC AAG CGG CGG AAT TGG TAC CCA AAA AAT GAA GAA GAT CAT	240
Met Arg Phe Lys Arg Arg Asn Trp Tyr Pro Lys Asn Glu Glu Asp His	
45 50 55 60	
AAG GCA TTA TCA GAA GCG GAT TGG GAG AAG TTA GGT GCG GGT AAG CCA	288
Lys Ala Leu Ser Glu Ala Asp Trp Glu Lys Leu Gly Ala Gly Lys Pro	
65 70 75	
GAT GAG TTT CCC CAA AGG AAT GAA ATA TTG AAT ATG ACT GAC GGA ATT	336
Asp Glu Phe Pro Gln Arg Asn Glu Ile Leu Asn Met Thr Asp Gly Ile	
80 85 90	
CTG AGT GAG TCT CTT CAG CTG GGT GAG GGC GGC AAA AGC CGC GTA GAA	384
Leu Ser Glu Ser Leu Gln Leu Gly Glu Gly Gly Lys Ser Arg Val Glu	
95 100 105	
GGA TAC ACG GAT TTC CAA TAT GTC CGC TCG GGC TAT ATC TAC CGC AAC	432
Gly Tyr Thr Asp Phe Gln Tyr Val Arg Ser Gly Tyr Ile Tyr Arg Asn	
110 115 120	
GGT GCC AAT AAA ATC GAT TTC CAA AAA AAA ATC GCC CTT TCC GGT CCG	480
Gly Ala Asn Lys Ile Asp Phe Gln Lys Lys Ile Ala Leu Ser Gly Pro	
125 130 135 140	
GAC GGC TAC CTT TTC TAC AAA GGC AGC AAT CCT TCC CAA GCT CTG CCG	528
Asp Gly Tyr Leu Phe Tyr Lys Gly Ser Asn Pro Ser Gln Ala Leu Pro	
145 150 155	
ATG GGT AAG GTA GGT TAT AAA GGT ACT TGG GAT TAT GTA ACC GAT GCC	576

Met	Gly	Lys	Val	Gly	Tyr	Lys	Gly	Thr	Trp	Asp	Tyr	Val	Thr	Asp	Ala	
			160					165					170			
AAG	ATG	GGA	CAA	AAA	TTT	TCC	CAG	TTG	GCT	GGT	TTT	CCA	GCG	GGG	GAT	624
Lys	Met	Gly	Gln	Lys	Phe	Ser	Gln	Leu	Ala	Gly	Phe	Pro	Ala	Gly	Asp	
		175					180					185				
AGG	TAT	GGG	GCT	TTG	TCT	GCC	GAG	GAA	GCG	GAT	GTG	TTG	CGC	AAC	AAA	672
Arg	Tyr	Gly	Ala	Leu	Ser	Ala	Glu	Glu	Ala	Asp	Val	Leu	Arg	Asn	Lys	
	190					195					200					
AGC	GAG	GCA	CAG	CAA	GGT	CAG	ACC	GAT	TTC	GGG	CTG	ACC	AGC	GAG	TTT	720
Ser	Glu	Ala	Gln	Gln	Gly	Gln	Thr	Asp	Phe	Gly	Leu	Thr	Ser	Glu	Phe	
205					210					215					220	
GAG	GTG	GAT	TTC	GCC	GCC	AAG	ACC	ATG	ACC	GGC	GCG	CTC	TAC	CGC	AAT	768
Glu	Val	Asp	Phe	Ala	Ala	Lys	Thr	Met	Thr	Gly	Ala	Leu	Tyr	Arg	Asn	
				225					230					235		
AAC	CGG	ATT	ACT	AAT	AAC	GAA	ACC	GAA	AAT	AAA	GCC	AAA	CAA	ATT	AAA	816
Asn	Arg	Ile	Thr	Asn	Asn	Glu	Thr	Glu	Asn	Lys	Ala	Lys	Gln	Ile	Lys	
			240					245					250			
CGT	TAC	GAC	ATT	CAG	GCT	GAC	CTG	CAC	GGT	AAC	CGC	TTC	AGC	GGC	AAG	864
Arg	Tyr	Asp	Ile	Gln	Ala	Asp	Leu	His	Gly	Asn	Arg	Phe	Ser	Gly	Lys	
		255					260					265				
GCA	ACG	GCA	ACC	GAC	AAA	CCC	AAA	AAC	GAC	GAA	ACC	AAG	GAA	CAT	CCC	912
Ala	Thr	Ala	Thr	Asp	Lys	Pro	Lys	Asn	Asp	Glu	Thr	Lys	Glu	His	Pro	
	270					275					280					
TTT	GTT	TCC	GAC	TCG	TCT	TCT	TTG	AGC	GGC	GGC	TTT	TTC	GGT	CCG	AAG	960
Phe	Val	Ser	Asp	Ser	Ser	Ser	Leu	Ser	Gly	Gly	Phe	Phe	Gly	Pro	Lys	
285					290					295					300	
GGT	GAG	GAA	TTG	GGT	TTC	CGC	TTT	TTG	AGC	GAC	GAT	CAA	AAA	GTT	GCC	1008
Gly	Glu	Glu	Leu	Gly	Phe	Arg	Phe	Leu	Ser	Asp	Asp	Gln	Lys	Val	Ala	
				305					310					315		
GTT	GTC	GGC	AGC	GCG	AAA	ACC	AAA	GAC	AAA	CTG	GAA	AAT	GGC	GCG	GCG	1056
Val	Val	Gly	Ser	Ala	Lys	Thr	Lys	Asp	Lys	Leu	Glu	Asn	Gly	Ala	Ala	
			320					325					330			
GCT	TCA	GGC	AGC	ACA	GGT	GCG	GCA	GCA	TCG	GGC	GGT	GCG	GCA	GAT	ATG	1104
Ala	Ser	Gly	Ser	Thr	Gly	Ala	Ala	Ala	Ser	Gly	Gly	Ala	Ala	Asp	Met	
		335					340					345				
CCG	TCT	GAA	AAC	GGT	AAG	CTG	ACC	ACG	GTT	TTG	GAT	GCG	GTT	GAG	CTG	1152
Pro	Ser	Glu	Asn	Gly	Lys	Leu	Thr	Thr	Val	Leu	Asp	Ala	Val	Glu	Leu	
		350				355					360					
AAA	TCT	GGC	GGT	AAG	GAA	GTC	AAA	AAT	CTC	GAC	AAC	TTC	AGC	AAT	GCC	1200
Lys	Ser	Gly	Gly	Lys	Glu	Val	Lys	Asn	Leu	Asp	Asn	Phe	Ser	Asn	Ala	
365					370					375					380	
GCC	CAA	CTG	GTT	GTC	GAC	GGC	ATT	ATG	ATT	CCG	CTC	CTG	CCC	AAG	AAT	1248
Ala	Gln	Leu	Val	Val	Asp	Gly	Ile	Met	Ile	Pro	Leu	Leu	Pro	Lys	Asn	
				385					390					395		
TCC	GAA	AGC	GAG	AGC	AAT	CAG	GCA	GAT	AAA	GGT	AAA	AAC	GGC	GGA	ACA	1296

Ser	Glu	Ser	Glu	Ser	Asn	Gln	Ala	Asp	Lys	Gly	Lys	Asn	Gly	Gly	Thr	
			400					405					410			
GCC Ala	TTT Phe	ACC Thr	CGC Arg	AAA Lys	TTT Phe	GAA Glu	CAC His	ACG Thr	CCG Pro	GAA Glu	AGT Ser	GAT Asp	AAA Lys	AAA Lys	GAC Asp	1344
		415					420					425				
ACC Thr	CAA Gln	GCA Ala	GGT Gly	ACG Thr	GCG Ala	GAG Glu	AAT Asn	GGC Gly	AAT Asn	CCA Pro	GCC Ala	GCT Ala	TCA Ser	AAT Asn	ACG Thr	1392
		430				435					440					
GCA Ala	GGT Gly	GAT Asp	ACC Thr	AAT Asn	GGC Gly	AAA Lys	ACA Thr	AAA Lys	ACC Thr	TAT Tyr	GAA Glu	GTC Val	GAA Glu	GTC Val	TGC Cys	1440
					450					455					460	
TGT Cys	TCC Ser	AAC Asn	CTC Leu	AAT Asn	TAT Tyr	CTG Leu	AAA Lys	TAC Tyr	GGA Gly	ATG Met	TTG Leu	ACG Thr	CGT Arg	AAA Lys	AAC Asn	1488
				465					470					475		
AGC Ser	AAG Lys	TCC Ser	GCG Ala	ATG Met	CAG Gln	GCA Ala	GGC Gly	GAA Glu	AAC Asn	GGT Gly	AGT Ser	CTA Leu	GCT Ala	GAC Asp	GCT Ala	1536
			480					485					490			
AAA Lys	ACG Thr	GAA Glu	CAA Gln	GTT Val	GAA Glu	CAA Gln	AGT Ser	ATG Met	TTC Phe	CTC Leu	CAA Gln	GGC Gly	GAG Glu	CGC Arg	ACC Thr	1584
		495					500					505				
GAT Asp	GAA Glu	AAA Lys	GAG Glu	ATT Ile	CCA Pro	AAA Lys	GAG Glu	CAA Gln	CAA Gln	GAC Asp	ATC Ile	GTT Val	TAT Tyr	CGG Arg	GGG Gly	1632
		510				515					520					
TCT Ser	TGG Trp	TAC Tyr	GGG Gly	CAT His	ATT Ile	GCC Ala	AAC Asn	GAC Asp	ACA Thr	AGC Ser	TGG Trp	AGC Ser	GGC Gly	AAT Asn	GCT Ala	1680
					530					535					540	
TCA Ser	GAT Asp	AGA Arg	GAG Glu	GGC Gly	GGC Gly	AAC Asn	AGG Arg	GCG Ala	GAC Asp	TTT Phe	ACC Thr	GTG Val	AAT Asn	TTT Phe	GGT Gly	1728
				545				550						555		
ACG Thr	AAA Lys	AAA Lys	ATT Ile	AAC Asn	GGA Gly	ACG Thr	TTA Leu	ACC Thr	GCT Ala	GAA Glu	AAC Asn	AGG Arg	CAG Gln	GAG Glu	GCA Ala	1776
			560					565					570			
ACC Thr	TTT Phe	ACC Thr	ATT Ile	GTG Val	GGC Gly	GAT Asp	ATT Ile	AAG Lys	GAC Asp	AAC Asn	GGC Gly	TTT Phe	GAA Glu	GGT Gly	ACG Thr	1824
		575					580					585				
GCG Ala	AAA Lys	ACT Thr	GCT Ala	GAC Asp	TCA Ser	GGT Gly	TTT Phe	GAT Asp	CTC Leu	GAT Asp	CAA Gln	AGC Ser	AAT Asn	ACC Thr	ACC Thr	1872
		590				595					600					
CGC Arg	ACG Thr	CCT Pro	AAG Lys	GCA Ala	TAT Tyr	ATC Ile	ACA Thr	GAT Asp	GCC Ala	AAG Lys	GTG Val	AAG Lys	GGC Gly	GGT Gly	TTT Phe	1920
					610					615					620	
TAC Tyr	GGG Gly	CCT Pro	AAA Lys	GCC Ala	GAA Glu	GAG Glu	TTG Leu	GGC Gly	GGA Gly	TGG Trp	TTT Phe	GCC Ala	TAT Tyr	CCG Pro	GGC Gly	1968
				625				630						635		
GAT Gly	AAA Lys	CAA Gln	ACG Arg	GAA Glu	AAG Lys	GCA Ala	ACG Arg	GTT Asp	ACA Thr	TCC Pro	GGC Gly	GAT Asp	GGA Glu	AAT Asn	TCA Ala	2016

Asp Lys Gln Thr Glu Lys Ala Thr Val Thr Ser Gly Asp Gly Asn Ser
640 645 650

GCA AGC AGT GCA ACT GTC GTA TTC GGT GCG AAA CGC CAA AAG CCT GTG 2064
Ala Ser Ser Ala Thr Val Val Phe Gly Ala Lys Arg Gln Lys Pro Val
655 660 665

CAA TAAAGTTTCG ATCTTGATTC TGTCGATACC GAAGCCCCGC GTCCCGCGCC AAATAAAA 2125
Gln

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 689 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe
-20 -15 -10 -5

Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser
1 5 10

Val Asp Thr Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser
15 20 25

Ser Glu Thr Pro Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala
30 35 40

Met Arg Phe Lys Arg Arg Asn Trp Tyr Pro Lys Asn Glu Glu Asp His
45 50 55 60

Lys Ala Leu Ser Glu Ala Asp Trp Glu Lys Leu Gly Ala Gly Lys Pro
65 70 75

Asp Glu Phe Pro Gln Arg Asn Glu Ile Leu Asn Met Thr Asp Gly Ile
80 85 90

Leu Ser Glu Ser Leu Gln Leu Gly Glu Gly Gly Lys Ser Arg Val Glu
95 100 105

Gly Tyr Thr Asp Phe Gln Tyr Val Arg Ser Gly Tyr Ile Tyr Arg Asn
110 115 120

Gly Ala Asn Lys Ile Asp Phe Gln Lys Lys Ile Ala Leu Ser Gly Pro
125 130 135 140

Asp Gly Tyr Leu Phe Tyr Lys Gly Ser Asn Pro Ser Gln Ala Leu Pro
145 150 155

Met Gly Lys Val Gly Tyr Lys Gly Thr Trp Asp Tyr Val Thr Asp Ala
160 165 170

Lys Met Gly Gln Lys Phe Ser Gln Leu Ala Gly Phe Pro Ala Gly Asp

135

175

180

185

Arg Tyr Gly Ala Leu Ser Ala Glu Glu Ala Asp Val Leu Arg Asn Lys
190 195 200

Ser Glu Ala Gln Gln Gly Gln Thr Asp Phe Gly Leu Thr Ser Glu Phe
205 210 215 220

Glu Val Asp Phe Ala Ala Lys Thr Met Thr Gly Ala Leu Tyr Arg Asn
225 230 235

Asn Arg Ile Thr Asn Asn Glu Thr Glu Asn Lys Ala Lys Gln Ile Lys
240 245 250

Arg Tyr Asp Ile Gln Ala Asp Leu His Gly Asn Arg Phe Ser Gly Lys
255 260 265

Ala Thr Ala Thr Asp Lys Pro Lys Asn Asp Glu Thr Lys Glu His Pro
270 275 280

Phe Val Ser Asp Ser Ser Ser Leu Ser Gly Gly Phe Phe Gly Pro Lys
285 290 295 300

Gly Glu Glu Leu Gly Phe Arg Phe Leu Ser Asp Asp Gln Lys Val Ala
305 310 315

Val Val Gly Ser Ala Lys Thr Lys Asp Lys Leu Glu Asn Gly Ala Ala
320 325 330

Ala Ser Gly Ser Thr Gly Ala Ala Ala Ser Gly Gly Ala Ala Asp Met
335 340 345

Pro Ser Glu Asn Gly Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu
350 355 360

Lys Ser Gly Gly Lys Glu Val Lys Asn Leu Asp Asn Phe Ser Asn Ala
365 370 375 380

Ala Gln Leu Val Val Asp Gly Ile Met Ile Pro Leu Leu Pro Lys Asn
385 390 395

Ser Glu Ser Glu Ser Asn Gln Ala Asp Lys Gly Lys Asn Gly Gly Thr
400 405 410

Ala Phe Thr Arg Lys Phe Glu His Thr Pro Glu Ser Asp Lys Lys Asp
415 420 425

Thr Gln Ala Gly Thr Ala Glu Asn Gly Asn Pro Ala Ala Ser Asn Thr
430 435 440

Ala Gly Asp Thr Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys
445 450 455 460

Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn
465 470 475

Ser Lys Ser Ala Met Gln Ala Gly Glu Asn Gly Ser Leu Ala Asp Ala
480 485 490

Lys Thr Glu Gln Val Glu Gln Ser Met Phe Leu Gln Gly Glu Arg Thr

495

500

505

Asp	Glu	Lys	Glu	Ile	Pro	Lys	Glu	Gln	Gln	Asp	Ile	Val	Tyr	Arg	Gly
510						515					520				
Ser	Trp	Tyr	Gly	His	Ile	Ala	Asn	Asp	Thr	Ser	Trp	Ser	Gly	Asn	Ala
525					530					535					540
Ser	Asp	Arg	Glu	Gly	Gly	Asn	Arg	Ala	Asp	Phe	Thr	Val	Asn	Phe	Gly
				545					550					555	
Thr	Lys	Lys	Ile	Asn	Gly	Thr	Leu	Thr	Ala	Glu	Asn	Arg	Gln	Glu	Ala
			560					565					570		
Thr	Phe	Thr	Ile	Val	Gly	Asp	Ile	Lys	Asp	Asn	Gly	Phe	Glu	Gly	Thr
		575					580					585			
Ala	Lys	Thr	Ala	Asp	Ser	Gly	Phe	Asp	Leu	Asp	Gln	Ser	Asn	Thr	Thr
	590					595					600				
Arg	Thr	Pro	Lys	Ala	Tyr	Ile	Thr	Asp	Ala	Lys	Val	Lys	Gly	Gly	Phe
605					610					615					620
Tyr	Gly	Pro	Lys	Ala	Glu	Glu	Leu	Gly	Gly	Trp	Phe	Ala	Tyr	Pro	Gly
				625					630					635	
Asp	Lys	Gln	Thr	Glu	Lys	Ala	Thr	Val	Thr	Ser	Gly	Asp	Gly	Asn	Ser
			640					645					650		
Ala	Ser	Ser	Ala	Thr	Val	Val	Phe	Gly	Ala	Lys	Arg	Gln	Lys	Pro	Val
		655					660					665			

Gln

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2143 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2133

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..60

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 61..2133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ATG Met -20	AAC Asn	AAT Asn	CCA Pro	TTG Leu	GTA Val -15	AAT Asn	CAG Gln	GCT Ala	GCT Ala	ATG Met -10	GTG Val	CTG Leu	CCT Pro	GTG Val	TTT Phe -5	48
TTG Leu	TTG Leu	AGT Ser	GCT Ala	TGT Cys 1	TTG Leu	GGC Gly	GGA Gly	GGC Gly 5	GGC Gly	AGT Ser	TTC Phe	GAT Asp	CTT Leu 10	GAT Asp	TCT Ser	96
GTC Val	GAT Asp	ACC Thr 15	GAA Glu	GCC Ala	CCG Pro	CGT Arg	CCC Pro 20	GCG Ala	CCA Pro	AAA Lys	TAT Tyr	CAA Gln 25	GAT Asp	GTT Val	TCT Ser	144
TCC Ser	GAA Glu 30	AAA Lys	CCG Pro	CAA Gln	GCC Ala	CAA Gln 35	AAA Lys	GAC Asp	CAA Gln	GGC Gly	GGA Gly 40	TAC Tyr	GGT Gly	TTT Phe	GCG Ala	192
ATG Met 45	AGG Arg	TTG Leu	AAA Lys	CGG Arg	AGG Arg 50	AAT Asn	CGG Arg	CAT His	CCG Pro	CAG Gln 55	GCA Ala	AAA Lys	GAA Glu	GAC Asp	AAA Lys 60	240
GTT Val	GAA Glu	CTA Leu	AAC Asn 65	CCA Pro	AAT Asn	GAT Asp	TGG Trp	GAG Glu 70	GAG Glu	ACA Thr	GGA Gly	TTG Leu	CCG Pro	AGC Ser 75	AAG Lys	288
CCC Pro	CAA Gln	AAC Asn 80	TTA Leu	CCC Pro	GAG Glu	CGA Arg	CAG Gln 85	CAA Gln	TCG Ser	GTT Val	ATT Ile	GAT Asp	AAA Lys 90	GTA Val	AAA Lys	336
ACA Thr	GAC Asp 95	GAT Asp	GGC Gly	AGC Ser	AAT Asn	ATT Ile 100	TAC Tyr	ACT Thr	TCC Ser	CCT Pro	TAT Tyr	CTC Leu 105	ACG Thr	CAA Gln	TCA Ser	384
AAC Asn 110	CAT His	CAA Gln	AAC Asn	GGC Gly	AGC Ser	ACT Thr 115	AAT Asn	AGC Ser	GGT Gly	GCA Ala	AAC Asn 120	CAA Gln	CCA Pro	AAA Lys	AAC Asn	432
GAA Glu 125	GTA Val	AAA Lys	GAT Asp	TAC Tyr 130	AAA Lys	AAT Asn	TTC Phe	AAA Lys	TAT Tyr	GTT Val 135	TAT Tyr	TCC Ser	GGC Gly	TGG Trp	TTT Phe 140	480
TAT Tyr	AAA Lys	CAT His	GCA Ala 145	GAG Glu	AGT Ser	GAA Glu	AGA Arg	GAA Glu 150	TTC Phe	AGT Ser	AAA Lys	ATC Ile	AAA Lys	TTT Phe 155	AAG Lys	528
TCA Ser	GGC Gly	GAC Asp 160	GAC Asp	GGC Gly	TAT Tyr	ATT Ile	TTT Phe 165	TAT Tyr	CAC His	GGT Gly	AAA Lys	GAC Asp	CCT Pro 170	TCC Ser	CGA Arg	576
CAA Gln	CTT Leu 175	CCC Pro	ACT Thr	TCT Ser	GAA Glu	AAA Lys	GTT Val 180	ATC Ile	TAC Tyr	AAA Lys	GGC Gly	GTA Val 185	TGG Trp	CAT His	TTT Phe	624
GTA Val 190	ACC Thr	GAT Asp	ACT Thr	GAA Glu	AAG Lys	GGA Gly 195	CAA Gln	AAA Lys	TTT Phe	AAC Asn 200	GAT Asp	ATT Ile	CTT Leu	GAA Glu	ACC Thr	672
TCA Ser 205	AAA Lys	GGG Gly	CAA Gln	GGC Gly	GAC Asp 210	AGA Arg	TAC Tyr	AGC Ser	GGA Gly	TTT Phe 215	TCG Ser	GGC Gly	GAT Asp	GAC Asp	GGC Gly 220	720

GAA Glu	ACA Thr	ACT Thr	TCC Ser	AAT Asn 225	AGA Arg	ACT Thr	GAT Asp	TCC Ser	AAC Asn 230	CTT Leu	AAT Asn	GAT Asp	AAG Lys	CAC His 235	GAG Glu	768
GGT Gly	TAT Tyr	GGT Gly	TTT Phe 240	ACC Thr	TCG Ser	AAT Asn	TTA Leu	GAA Glu 245	GTG Val	GAT Asp	TTC Phe	GGC Gly	AGT Ser 250	AAA Lys	AAA Lys	816
TTG Leu	ACG Thr	GGT Gly 255	AAA Lys	TTA Leu	ATA Ile	CGC Arg	AAT Asn 260	AAT Asn	AGA Arg	GTT Val	ACA Thr	AAC Asn 265	GCT Ala	ACT Thr	ACT Thr	864
AAC Asn 270	GAT Asp	AAA Lys	TAC Tyr	ACC Thr	ACC Thr	CAA Gln 275	TAC Tyr	TAC Tyr	AGC Ser	CTT Leu	GAT Asp 280	GCC Ala	CAA Gln	ATA Ile	ACA Thr	912
GGC Gly 285	AAC Asn	CGC Arg	TTC Phe	AAC Asn 290	GGT Gly	AAG Lys	GCG Ala	ATA Ile	GCG Ala	ACC Thr 295	GAC Asp	AAA Lys	CCC Pro	GAC Asp	ACT Thr 300	960
GGA Gly	GGA Gly	ACC Thr	AAA Lys	CTA Leu 305	CAT His	CCC Pro	TTT Phe	GTT Val	TCC Ser 310	GAC Asp	TCG Ser	TCT Ser	TCT Ser	TTG Leu 315	AGC Ser	1008
GGC Gly	GGC Gly	TTT Phe	TTC Phe 320	GGT Gly	CCG Pro	AAG Lys	GGT Gly	GAG Glu 325	GAA Glu	TTG Leu	GGT Gly	TTC Phe	CGC Arg 330	TTT Phe	TTG Leu	1056
AGC Ser	GAC Asp	GAT Asp 335	AAA Lys	AAA Lys	GTT Val	GCG Ala	GTT Val 340	GTC Val	GGC Gly	AGC Ser	GCG Ala	AAA Lys 345	ACC Thr	AAA Lys	GAC Asp	1104
AAA Lys 350	ACG Thr	GAA Glu	AAT Asn	GGC Gly	GCG Ala	GTG Val 355	GCT Ala	TCA Ser	GGC Gly	GGC Gly	ACA Thr 360	GAT Asp	GCG Ala	GCA Ala	GCA Ala	1152
TCA Ser 365	AAC Asn	GGT Gly	GCG Ala	GCA Ala	GGC Gly 370	ACG Thr	TCG Ser	TCT Ser	GAA Glu	AAC Asn 375	AGT Ser	AAG Lys	CTG Leu	ACC Thr	ACG Thr 380	1200
GTT Val	TTG Leu	GAT Asp	GCG Ala	GTC Val 385	GAG Glu	CTG Leu	AAA Lys	TTG Leu	GGC Gly 390	GAT Asp	AAG Lys	GAA Glu	GTC Val	CAA Gln 395	AAG Lys	1248
CTC Leu	GAC Asp	AAC Asn	TTC Phe 400	AGC Ser	AAC Asn	GCC Ala	GCC Ala	CAA Gln 405	CTG Leu	GTT Val	GTC Val	GAC Asp	GGC Gly 410	ATT Ile	ATG Met	1296
ATT Ile	CCG Pro	CTC Leu 415	TTG Leu	CCC Pro	GAG Glu	ACT Thr	TCC Ser 420	GAA Glu	AGT Ser	GGG Gly	AAC Asn 425	AAT Asn	CAA Gln	GCC Ala	AAT Asn	1344
CAA Gln 430	GGT Gly	ACA Thr	AAT Asn	GGC Gly	GGA Gly	ACA Thr 435	GCC Ala	TTT Phe	ACC Thr	CGC Arg	AAA Lys 440	TTT Phe	GAC Asp	CAC His	ACG Thr	1392
CCG Pro 445	GAA Glu	AGT Ser	GAT Asp	AAA Lys 450	AAA Lys	GAC Asp	GCC Ala	CAA Gln	GCA Ala	GGT Gly 455	ACG Thr	CAG Gln	ACG Thr	AAT Asn	GGG Gly 460	1440

GCG CAA ACC GCT TCA AAT ACG GCA GGT GAT ACC AAT GGC AAA ACA AAA	1488
Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys Thr Lys	
465 470 475	
ACC TAT GAA GTC GAA GTC TGC TGT TCC AAC CTC AAT TAT CTG AAA TAC	1536
Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr	
480 485 490	
GGA ATG TTG ACG CGC AAA AAC AGC AAG TCC GCG ATG CAG GCA GGA GAA	1584
Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Glu	
495 500 505	
AGC AGT AGT CAA GCT GAT GCT AAA ACG GAA CAA GTT GGA CAA AGT ATG	1632
Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Gly Gln Ser Met	
510 515 520	
TTC CTC CAA GGC GAG CGC ACC GAT GAA AAA GAG ATT CCA AGC GAG CAA	1680
Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Ser Glu Gln	
525 530 535 540	
AAC ATC GTT TAT CGG GGG TCT TGG TAC GGG CAT ATT GCC AGC AGC ACA	1728
Asn Ile Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Ser Ser Thr	
545 550 555	
AGC TGG AGC GGC AAT GCT TCT GAT AAA GAG GGC GGC AAC AGG GCG GAA	1776
Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn Arg Ala Glu	
560 565 570	
TTT ACT GTG AAT TTT GGC GAG AAA AAA ATT ACC GGC ACG TTA ACC GCT	1824
Phe Thr Val Asn Phe Gly Glu Lys Lys Ile Thr Gly Thr Leu Thr Ala	
575 580 585	
GAA AAC AGG CAG GAG GCA ACC TTT ACC ATT GAT GGT AAG ATT GAG GGC	1872
Glu Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp Gly Lys Ile Glu Gly	
590 595 600	
AAC GGT TTT TCC GGT ACG GCA AAA ACT GCT GAA TTA GGT TTT GAT CTC	1920
Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Glu Leu Gly Phe Asp Leu	
605 610 615 620	
GAT CAA AAA AAT ACC ACC CGC ACG CCT AAG GCA TAT ATC ACA GAT GCC	1968
Asp Gln Lys Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala	
625 630 635	
AAG GTG CAG GGC GGT TTT TAC GGG CCC AAA GCC GAA GAG TTG GGC GGA	2016
Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly	
640 645 650	
TGG TTT GCC TAT CAG GGC GAT AAA CAA ACG GAA AAT ACA ACA GTT GCA	2064
Trp Phe Ala Tyr Gln Gly Asp Lys Gln Thr Glu Asn Thr Thr Val Ala	
655 660 665	
TCC GGC AAT GGA AAT TCA GCA AGC AGT GCA ACT GTC GTA TTC GGT GCG	2112
Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala Thr Val Val Phe Gly Ala	
670 675 680	
AAA CGC CAA AAG CCT GTG CAA TAAAGTAAAA	2143
Lys Arg Gln Lys Pro Val Gln	
685 690	

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe
-20 -15 -10 -5

Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser
1 5 10

Val Asp Thr Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser
15 20 25

Ser Glu Lys Pro Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala
30 35 40

Met Arg Leu Lys Arg Arg Asn Arg His Pro Gln Ala Lys Glu Asp Lys
45 50 55 60

Val Glu Leu Asn Pro Asn Asp Trp Glu Glu Thr Gly Leu Pro Ser Lys
65 70 75

Pro Gln Asn Leu Pro Glu Arg Gln Gln Ser Val Ile Asp Lys Val Lys
80 85 90

Thr Asp Asp Gly Ser Asn Ile Tyr Thr Ser Pro Tyr Leu Thr Gln Ser
95 100 105

Asn His Gln Asn Gly Ser Thr Asn Ser Gly Ala Asn Gln Pro Lys Asn
110 115 120

Glu Val Lys Asp Tyr Lys Asn Phe Lys Tyr Val Tyr Ser Gly Trp Phe
125 130 135 140

Tyr Lys His Ala Glu Ser Glu Arg Glu Phe Ser Lys Ile Lys Phe Lys
145 150 155

Ser Gly Asp Asp Gly Tyr Ile Phe Tyr His Gly Lys Asp Pro Ser Arg
160 165 170

Gln Leu Pro Thr Ser Glu Lys Val Ile Tyr Lys Gly Val Trp His Phe
175 180 185

Val Thr Asp Thr Glu Lys Gly Gln Lys Phe Asn Asp Ile Leu Glu Thr
190 195 200

Ser Lys Gly Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp Asp Gly
205 210 215 220

Glu Thr Thr Ser Asn Arg Thr Asp Ser Asn Leu Asn Asp Lys His Glu
225 230 235

Gly	Tyr	Gly	Phe	Thr	Ser	Asn	Leu	Glu	Val	Asp	Phe	Gly	Ser	Lys	Lys	240	245	250
Leu	Thr	Gly	Lys	Leu	Ile	Arg	Asn	Asn	Arg	Val	Thr	Asn	Ala	Thr	Thr	255	260	265
Asn	Asp	Lys	Tyr	Thr	Thr	Gln	Tyr	Tyr	Ser	Leu	Asp	Ala	Gln	Ile	Thr	270	275	280
Gly	Asn	Arg	Phe	Asn	Gly	Lys	Ala	Ile	Ala	Thr	Asp	Lys	Pro	Asp	Thr	285	290	300
Gly	Gly	Thr	Lys	Leu	His	Pro	Phe	Val	Ser	Asp	Ser	Ser	Ser	Leu	Ser	305	310	315
Gly	Gly	Phe	Phe	Gly	Pro	Lys	Gly	Glu	Glu	Leu	Gly	Phe	Arg	Phe	Leu	320	325	330
Ser	Asp	Asp	Lys	Lys	Val	Ala	Val	Val	Gly	Ser	Ala	Lys	Thr	Lys	Asp	335	340	345
Lys	Thr	Glu	Asn	Gly	Ala	Val	Ala	Ser	Gly	Gly	Thr	Asp	Ala	Ala	Ala	350	355	360
Ser	Asn	Gly	Ala	Ala	Gly	Thr	Ser	Ser	Glu	Asn	Ser	Lys	Leu	Thr	Thr	365	370	375
Val	Leu	Asp	Ala	Val	Glu	Leu	Lys	Leu	Gly	Asp	Lys	Glu	Val	Gln	Lys	385	390	395
Leu	Asp	Asn	Phe	Ser	Asn	Ala	Ala	Gln	Leu	Val	Val	Asp	Gly	Ile	Met	400	405	410
Ile	Pro	Leu	Leu	Pro	Glu	Thr	Ser	Glu	Ser	Gly	Asn	Asn	Gln	Ala	Asn	415	420	425
Gln	Gly	Thr	Asn	Gly	Gly	Thr	Ala	Phe	Thr	Arg	Lys	Phe	Asp	His	Thr	430	435	440
Pro	Glu	Ser	Asp	Lys	Lys	Asp	Ala	Gln	Ala	Gly	Thr	Gln	Thr	Asn	Gly	445	450	455
Ala	Gln	Thr	Ala	Ser	Asn	Thr	Ala	Gly	Asp	Thr	Asn	Gly	Lys	Thr	Lys	465	470	475
Thr	Tyr	Glu	Val	Glu	Val	Cys	Cys	Ser	Asn	Leu	Asn	Tyr	Leu	Lys	Tyr	480	485	490
Gly	Met	Leu	Thr	Arg	Lys	Asn	Ser	Lys	Ser	Ala	Met	Gln	Ala	Gly	Glu	495	500	505
Ser	Ser	Ser	Gln	Ala	Asp	Ala	Lys	Thr	Glu	Gln	Val	Gly	Gln	Ser	Met	510	515	520
Phe	Leu	Gln	Gly	Glu	Arg	Thr	Asp	Glu	Lys	Glu	Ile	Pro	Ser	Glu	Gln	525	530	535
Asn	Ile	Val	Tyr	Arg	Gly	Ser	Trp	Tyr	Gly	His	Ile	Ala	Ser	Ser	Thr	545	550	555

Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn Arg Ala Glu
 560 565 570
 Phe Thr Val Asn Phe Gly Glu Lys Lys Ile Thr Gly Thr Leu Thr Ala
 575 580 585
 Glu Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp Gly Lys Ile Glu Gly
 590 595 600
 Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Glu Leu Gly Phe Asp Leu
 605 610 615 620
 Asp Gln Lys Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala
 625 630 635
 Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly
 640 645 650
 Trp Phe Ala Tyr Gln Gly Asp Lys Gln Thr Glu Asn Thr Thr Val Ala
 655 660 665
 Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala Thr Val Val Phe Gly Ala
 670 675 680
 Lys Arg Gln Lys Pro Val Gln
 685 690

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Thr Lys Asp Lys Leu Glu Asn Gly Ala Ala Ala Ser Gly Ser Thr Gly
 1 5 10 15
 Ala Ala Ala Ser Gly Gly Ala Ala Asp Met Pro Ser Glu Asn Gly Lys
 20 25 30
 Leu Thr Thr Val Leu Asp Ala Val Glu Leu Lys Ser Gly Gly Lys Glu
 35 40 45
 Val Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
 50 55 60
 Gly Ile Met Ile Pro Leu Leu Pro Lys Asn Ser Glu Ser Glu Ser Asn
 65 70 75 80
 Gln Ala Asp Lys Gly Lys Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
 85 90 95

Glu His Thr Pro Glu Ser Asp Lys Lys Asp Thr Gln Ala Gly Thr Ala
 100 105 110
 Glu Asn Gly Asn Pro Ala Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
 115 120 125
 Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
 130 135 140
 Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln
 145 150 155 160
 Ala Gly Glu Asn Gly Ser Leu Ala Asp Ala Lys Thr Glu Gln Val Glu
 165 170 175
 Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro
 180 185 190
 Lys Glu Gln Gln Asp Ile Val
 195

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Thr Lys Asp Lys Thr Glu Asn Gly Ala Val Ala Ser Gly Gly Thr Asp
 1 5 10 15
 Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys
 20 25 30
 Leu Thr Thr Val Leu Asp Ala Val Glu Leu Lys Leu Gly Asp Lys Glu
 35 40 45
 Val Gln Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
 50 55 60
 Gly Ile Met Ile Pro Leu Leu Pro Glu Thr Ser Glu Ser Gly Asn Asn
 65 70 75 80
 Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
 85 90 95
 Asp His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln
 100 105 110
 Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
 115 120 125

144

Lys	Thr	Lys	Thr	Tyr	Glu	Val	Glu	Val	Cys	Cys	Ser	Asn	Leu	Asn	Tyr
130						135					140				
Leu	Lys	Tyr	Gly	Met	Leu	Thr	Arg	Lys	Asn	Ser	Lys	Ser	Ala	Met	Gln
145					150					155					160
Ala	Gly	Glu	Ser	Ser	Ser	Gln	Ala	Asp	Ala	Lys	Thr	Glu	Gln	Val	Gly
				165					170					175	
Gln	Ser	Met	Phe	Leu	Gln	Gly	Glu	Arg	Thr	Asp	Glu	Lys	Glu	Ile	Pro
			180					185					190		
Ser	Glu	Gln	Asn	Ile	Val										
			195												

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Thr	Lys	Asp	Asn	Thr	Ala	Asn	Gly	Asn	Thr	Ala	Ala	Ala	Ser	Gly	Gly
1				5					10					15	
Thr	Asp	Ala	Ala	Ala	Ser	Asn	Gly	Ala	Ala	Gly	Thr	Ser	Ser	Glu	Asn
		20						25					30		
Gly	Lys	Leu	Thr	Thr	Val	Leu	Asp	Ala	Val	Glu	Leu	Thr	Leu	Asn	Asp
		35					40					45			
Lys	Lys	Ile	Lys	Asn	Leu	Asp	Asn	Phe	Ser	Asn	Ala	Ala	Gln	Leu	Val
		50				55					60				
Val	Asp	Gly	Ile	Met	Ile	Pro	Leu	Leu	Pro	Glu	Ala	Ser	Glu	Ser	Gly
65					70					75					80
Asn	Asn	Gln	Ala	Asn	Gln	Gly	Thr	Asn	Gly	Gly	Thr	Ala	Phe	Thr	Arg
				85					90					95	
Lys	Phe	Ala	His	Thr	Pro	Lys	Ser	Asp	Glu	Lys	Asp	Thr	His	Ala	Gly
			100					105					110		
Thr	Ala	Ala	Asn	Gly	Asp	Gln	Ala	Ala	Ser	Asn	Thr	Ala	Gly	Asp	Thr
			115				120					125			
Asn	Gly	Lys	Thr	Lys	Thr	Tyr	Glu	Val	Glu	Val	Cys	Cys	Ser	Asn	Leu
		130				135					140				
Asn	Tyr	Leu	Lys	Tyr	Gly	Leu	Leu	Thr	Arg	Lys	Thr	Ala	Gly	Asn	Thr
145					150					155					160

145

Gly Glu Gly Gly Asn Gly Ser Gln Thr Ala Ala Ala Gln Thr Ala Gln
165 170 175
Gly Ala Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu
180 185 190
Ile Pro Ser Glu Gln Asn Val
195

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Gly Phe Tyr Gly Pro Lys Gly Glu
1 5

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Gly Phe Tyr Gly Lys Asn Ala Ile
1 5

146